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            GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on:     August 28, 2002, 08:35:50 ; Search time 283.89 Seconds
                                         (without alignments)
                                         15204.299 Million cell updates/sec

Title:      US-08-711-417C-165
Perfect score: 1551
Sequence:   1 ATGGATGCTGACCAGGTCA.........ACCGCTTCCACATGAGCTAA 1551

Scoring table: IDENTITY.NUC
            Gapop 10.0 , Gapext 1.0

Searched:   1759959 seqs, 1391472711 residues

Total number of hits satisfying chosen parameters:     3519918

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  Pending_Patents_NA_New:*
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            2: /cgn2_6/ptodata/1/pna/US06_NEW_COMB.seq:*
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            5: /cgn2_6/ptodata/1/pna/US09_NEW_COMB.seq:*
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            8: /cgn2_6/ptodata/1/pna/US60_NEW_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                        SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	1468.8	94.7	1560	6	US-10-035-832-1162	Sequence 1162, Ap
2	1468.8	94.7	3629	5	US-09-442-384B-721	Sequence 721, App
3	1468.8	94.7	3629	5	US-10-035-832-1161	Sequence 1161, Ap
4	1456.2	93.9	6280	1	PCT-US02-09944-258	Sequence 258, App
5	1386	89.4	1386	4	US-08-733-622C-16	Sequence 16, Appl
6	1174.8	75.7	2049	4	US-08-733-622C-18	Sequence 18, Appl
7	868	56.0	1004	4	US-08-733-622C-21	Sequence 21, Appl
8	814.8	52.5	1296	6	US-10-035-832-1159	Sequence 1159, Ap
9	814.8	52.5	1550	6	US-09-053-375B-942	Sequence 942, App
10	814.8	52.5	1550	6	US-10-035-832-1158	Sequence 1158, Ap
11	813.2	52.4	1788	4	US-08-733-622C-15	Sequence 15, Appl
12	689.4	44.4	1296	4	US-08-733-622C-17	Sequence 17, Appl
13	577	37.2	1170	4	US-08-733-622C-19	Sequence 19, Appl
14	479.2	30.9	87977	6	US-10-035-832-1157	Sequence 1157, Ap
15	458.2	29.5	1128	4	US-08-733-622C-20	Sequence 20, Appl
16	416.2	26.8	2453	6	US-10-198-846-13080	Sequence 13080, A
17	411.8	26.6	1984	4	US-08-733-622C-1	Sequence 1, Appli
18	263	17.0	96594	6	US-10-035-832-1160	Sequence 1160, Ap
19	229	14.8	229	5	US-09-442-366A-1259	Sequence 1259, Ap
20	228	14.7	228	5	US-09-442-384B-306	Sequence 306, App
21	216.4	14.0	628	4	US-08-733-622C-7	Sequence 7, Appli
22	130	8.4	620	5	US-09-785-276A-59291	Sequence 59291, A
c 23	96.2	6.2	656	6	US-10-216-086-6	Sequence 6, Appli
24	95.2	6.1	2150	5	US-09-889-616A-99	Sequence 99, Appl
25	87.8	5.7	478	5	US-09-918-995-20176	Sequence 20176, A

26	87.8	5.7	2961	5	US-09-785-276A-24131	Sequence 24131, A
27	87.8	5.7	2961	5	US-09-785-276A-25903	Sequence 25903, A
28	87.8	5.7	2961	5	US-09-785-276A-30131	Sequence 30131, A
29	87.6	5.7	4124	6	US-10-198-846-9813	Sequence 9813, Ap
30	87.6	5.6	2627	7	US-10-157-031-35	Sequence 35, Appl
31	87.2	5.6	3727	5	US-09-620-325-229	Sequence 229, App
32	87.2	5.6	1823	9	PCT-US02-2179-59	Sequence 59, Appl
33 c	87.2	5.6	1909	8	US-60-365-384-484	Sequence 484, App
34	87.2	5.6	2253	1	PCT-US02-2179-60	Sequence 60, Appl
35	87.2	5.6	2321	7	US-10-104-047-888	Sequence 888, App
36	87.2	5.6	2547	8	US-60-365-384-145	Sequence 145, App
37 c	87.2	5.6	6511	6	US-10-212-872-1066	Sequence 1066, Ap
38 c	87.2	5.6	6511	6	US-10-212-872-1072	Sequence 1072, Ap
39 c	87.2	5.6	9316	6	US-10-212-872-1071	Sequence 1071, Ap
40 c	87.2	5.6	10061	6	US-10-212-872-1069	Sequence 1069, Ap
41 c	87.2	5.6	128779	5	US-10-081-327A-38	Sequence 38, Appl
42	87	5.6	461	5	US-09-918-995-22715	Sequence 22715, A
43	85.4	5.5	2543	5	US-09-629-469A-12347	Sequence 12347, A
44	85.4	5.5	3048	5	US-09-629-469A-11980	Sequence 11980, A
45	85.2	5.5	458	5	US-09-918-995-701	Sequence 701, App

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                        ALIGNMENTS

RESULT 1
US-10-035-832-1162
; Sequence 1162, Application US/10035832
; GENERAL INFORMATION:
;  APPLICANT: Morris, David
;  APPLICANT: Engelhard, Eric
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: A-7124S/RMS/DCF
;  CURRENT APPLICATION NUMBER: US/10/035,832
;  CURRENT FILING DATE: 2002-07-22
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1613
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 1162
;  LENGTH: 1560
;  TYPE: DNA
;  ORGANISM: Homo sapiens
US-10-035-832-1162

Query Match             94.7%;  Score 1468.8;  DB 6;  Length 1560;
Best Local Similarity   97.7%;  Pred. No. 0;
Matches 1524;  Conservative  0;  Mismatches 27;  Indels  9;  Gaps  3;

Qy      1 ATGGATGCTGACGAGGGTCAAGACACATGTCTTTCTCATCAGGGAAGGAAAGCCCCCTGTA 60
          |||||||||| |||||||||| |||||||||                   ||||||||||||
Db      1 atggatgctgatgagggtcaagacacatgtcccaagttcaggggaaggaaagcccccctgta 60

Qy     61 AGGGATACTCCAGATGAGGGCGATGAGCCACCATGCCCGATCCCCGAGGACCTCTCCACACC 120
          |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Db     61 agcgatactccagatgagggcgatgagcccatgcgatccccgagtccccgaggacctctccacacc 120

Qy    121 TCGGGAGGACAGCAAAGCTCAAAGAGTGACAGAGTCGTGGCCAGTAATGTTAAAGTAGAG 180
          |||||||||||||| |||||||||||||||||| |||||||||||||||| ||||
Db    121 tcgggaggacagcagcaaagctccaagagtgacagagtcgtggccagtaatgttaaagtagag 180

Qy    181 ACTCAGAGTGATGAAGAGAATGGGCGTCCTGTGAAATGAATGAGGGGAAGAATGTGCGGAG 240
          ||||||||||||||||||||||||||||||||||||||||                ||||||||
Db    181 actcagagtgatgaagagaatgggcgtgcctgtgaaatgaatggggaagaatgtgcggag 240

Qy    241 GATTTACGAAATGCTTGATGCCTCGGGAGGAGAAAATGAATGCTCCCACAGGGACCAAGGC 300
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 gattacgaatgtcttgatgcctcggggaggagaaaatgaatggctcccacagggggaccaaggc 300

Qy    301 AGCTCGGCTTTGTCGGGAGTTGGAGCATTCGACTTCCTAACGGAAAACTAAAGTGTGAT 360
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Db  1381 gtgtacaagtgcgaacactgccggtgtctcctcggatcacgtcatgtacaccatccac 1440
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Qy  1432 ATGGGCTGCCACGGCTTCCGTGCTCGTCTTTGAGTGCAACAATGTGCGGCTACCAGCCAG 1491
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1441 atgggctgccacggcttccgtgctccttgagtgcaacatgtggctaccacagccag 1500
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Qy  1492 GACCGGTACGAGTTCTCTCGCACATAACGCCAGGGGAGCACCGCTTCCACATGAGCTAA 1551
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Db  1501 gaccggtacgagttctcgtcgcacataacgcgaggggagcaccgctccactgagctaa 1560


RESULT  2
US-09-442-384B-721
; Sequence 721, Application US/09442384B
; GENERAL INFORMATION:
;  APPLICANT: Chenchik, Alex
;  APPLICANT: Lukashev, Matvey
;  TITLE OF INVENTION: Hematology/Immunology Array
;  FILE REFERENCE: CLON-006CIP15
;  CURRENT APPLICATION NUMBER: US/09/442,384B
;  CURRENT FILING DATE: 1999-11-17
;  PRIOR APPLICATION NUMBER: 09/053,375
;  PRIOR FILING DATE: 1998-03-31
;  NUMBER OF SEQ ID NOS: 830
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 721
;  LENGTH: 3629
;  TYPE: DNA
;  ORGANISM: homo sapiens
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: 3078
;  OTHER INFORMATION: n = A,T,C or G
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: 3078
;  OTHER INFORMATION: n = A,T,C or G
US-09-442-384B-721

Query Match             94.7%;   Score 1468.8;  DB 5;  Length 3629;
Best Local Similarity   97.7%;   Pred. No. 0;
Matches 1524;  Conservative     0;  Mismatches    27;  Indels     9;  Gaps     3;

Qy     1 ATGGATGCTGACGAGGTCAAGACATGTCTTTCTCATCAGGAGGAAGAAGCCCCCTGTA 60
              |||||||||| ||||||| |||||||||||||||||||||||||||||||||||||||
Db   169 atggatgctgagtagggtcaagacatgtcccaagtttcagggaggaaagcccccctgta 228
Qy    61 AGCGATACTCCAGATGAGGGCGATGAGCCCATGCGCATCCCGAGGCACCTCTCCACCACC 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   229 agcgatactccagatgagggcgatgagcccatgcgcatcccgaggcacctctccaccacc 288
Qy   121 TCGGGAGCAGCAAAGCTCCAAGAGTCGTGCCAGTAAATGTTAAAGTAGAG 180
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Db   289 tcgggaggacagcagcaagctccaagagtcgtggccagtaatgttaaagtagag 348
Qy   181 ACTCAGAGTGATGAAGAAGAATGGGCCTGTCCTGTGAAATGAATGGGAGAGAAATATGTCGGAG 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   349 actcagagtgatgaagagaatgggctgtcctgtgaaatgaatgatgggggaggaatgtgtcggag 408
Qy   241 GATTTACGAATGCTTGATGCCTCCGGAGAGAAAAATAAAGTGTGAT 300
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Db   409 gatttacgaatgcttgatgcctcggagagaaaatgaatggctcctaacggacaaactaaagtgtgat 468
Qy   301 AGCTCGGCTTTGTCGGGAGTTGGAGCATTCGACTTCCTAACGGAAAACTAAAGTGTGAT 360
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Db   469 agctcggcttcgtcgggagttggaggcattcgacttcctaacggaaaactaaagtgtgat 528
Qy   361 ATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGGTTCACAAAAGAGACCACACT 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   529 atctgtgggatcatttgcatcgggcccaatgtgctcatggttcacaaaagaagccacact 588
Qy   421 GGAGAACGGCGCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACCCAGAAGAGGCAACCTG 480
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Db   1669 gaccggtacgagttctgtcgcacataacgcgagggagcaccgcttccacatgagctaa 1728

RESULT 3
US-10-035-832-1161
; Sequence 1161, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1161
; LENGTH: 3629
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3078)..(3078)
; OTHER INFORMATION: "n" at position 3078 can be any base
US-10-035-832-1161

Query Match   94.7%; Score 1468.8; DB 6; Length 3629;
Best Local Similarity   97.7%; Pred. No. 0;
Matches 1524; Conservative 0; Mismatches 27; Indels 9; Gaps 3;

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Db   169 atggatgctgatgaggtcaagacatgtcccaagtttcagggaaggaaagccccccgtta 228

Qy   61 AGCGGATACTCCAGATGAGGGCGATGAGCCCATGCGCGACCTCTCCACCACC 120
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Db   229 agcgatactccagatgagggcgatgagcccatgcgcgacctctccaccacc 288

Qy   121 TCGGGAGGACAGCAAAGCTCCAAGAGTGACAGAGTCGTGGCCAGTAATGTTAAAGTAGAG 180
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Db   289 tcgggaggacagcaaagctccaagagtgacagagtcgtggccagtaatgttaaagtagag 348

Qy   181 ACTCAGAGTGATGAAGAGAATGGCGTGCCTGTGAAATGAAATGAATGATGGGGAAGAATGCGCGAG 240
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Qy   241 GATTTACGAATGCTTGATGCCTCGGGACAGAGAAAATGAATGGCTCCCAGGACCAAGGC 300
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Db   469 agctcggcttgtcgggagttggaggcattcgacttcctaacgagaaactaaagtgtgat 528

Qy   361 ATCTGTGGGATCATTTGCATCGGGCCCAATGTGCGGGGCCTCATTCACCCAGAGATGAAG 420
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Db   529 atctgtgggatcatttgcatcgggcccaatgtgcggggcctcattcacccagagatgaag 588

Qy   421 GGAGAACGGCCCTCCAGTGCAATCAGTGCGGGGCCTCATTCACCCAGAAGGGCAACCTG 480
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Qy   481 CTCCGGCACACTCAAGCTGCATTCCGGGAGAAGCCCTTCAAATGCCACTCTCGCAACTAC 540
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Db   649 ctccggcacatcaagctgcattccgggagaagcccttcaaatgccactctcgcaactac 708

Qy   541 GCCTGCCGCCGGAGGGACGGCCCTCACTGGCCACCTGAGGACGACCACTCCGTTGGTAAACCT 600
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Db   709 gcctgccgccggagggacggcccctcactggccacctgaggacgactccgttggtaaacct 768

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Qy   481 CTCCGGCACATCAAGCTGCATTCCGGGAGAAGCCCTTCAAATGCCACTCTCGCAACTAC 540
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Qy   541 GCCTGCCGCCGGAGGGACGGCCCTCACTGGCCACCTGAGGACGACCACTCCGTTGGTAAACCT 600
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Qy   601 CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGAGGAACATAAA 660
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Db   769 cacaaatgtggatattggtggccgaagctataaacagcgaacataaa 828

Qy   661 GAGCGCGTGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCACACTGTACCCAGTCATT 720
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Qy   841 AAATTTCTTGGGGACAAGGGCCTGTCCGACACGCCCTACCA---CAGTGCCACGTACGAG 897
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Db   1009 aaatttcttggggacaagggcctgtccgacacgcccagcacagcgccagctacgag 1068

Qy   898 AAGGAGAACGAAATGATGAAGTCCCACGTGATGGACCAAGCCATCAACACGCCATCAAC 957
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Qy   958 TACCTGGGGCGGCCCAGTCCCTGCGCCCTGGTGCAGACGCCCCGGGCGGTTCCGAGTG 1017
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Qy   1018 GTCCCGGTCATCAGCCGATGTACCAGCTGCACA---GGCGCTCGGAGGCCACCCCCGCGC 1074
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Db   1189 gtcccggtcatcagccgatgtaccagctgcacagctcgggaggccacccccgcgc 1248

Qy   1075 TCCAACCACTCGGCCCAGGACAGCAGCGCCGTGGAGTCACCTGCTCTCCAAGGCCAAG 1134
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Db   1249 tccaaccactcggcccaggacagcagcgccgtggagtcacctgctctccaaggccaag 1308

Qy   1135 TTGGTGCCCTCGGAGCGCGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACC 1194
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Db   1309 ttggtgccctcggagcgcgaggcgtccccgagcaacagctgccaagactccacggacacc 1368

Qy   1195 GAGAGCAACAACGAGGAGGACGCAGCGGTCTTATCCTACCTGACCAACCACCACATCGCCCGA 1254
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Qy   1255 CGGCGC----AACGGTGTCGCTCAAGGAGGAGCACCGGCCTACGACCTGCTGCGCGCC 1311
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Db   1429 cacgccgagaactcgcaggacaacactcgagacctgctgcgcgcc 1488

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Db   1489 gcctccgagaactcgcaggacgcgccgggctgcctggtcagaccacgcacgcgcc 1548

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Db   1549 gtgtacaagtgcgaacactgccgggggctgtcttcctggatcacgtcatgtacaccatccac 1608

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Db   1609 atgggctgccacggcttccgtgatccttttgagtgcaacatgtgcggctaccagacccag 1668

Qy   1492 GACCGGTACGAGTTCTCTGTCGCCACATAAACGCGAGGGGAGCACCGCTTCCACATGAGCTAA 1551
          |||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 gaccggtacgagttctctgtcgccacataaacgcgaggggagcaccgctttggtaaacct 1551

APPLICANT: TRAN, Alanna-Phung B.
APPLICANT: DAHL, Christopher R.
APPLICANT: GIETZEN, Darryl
APPLICANT: CHINN, Joyce
APPLICANT: DUFOUR, Gerard E.
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: YU, Jimmy Y.
APPLICANT: TUASON, Olivia
APPLICANT: YAP, Pierre E.
APPLICANT: AMSHEY, Stefan R.
APPLICANT: DAUGHERTY, Sean C.
APPLICANT: DAM, Tam C.
APPLICANT: LIU, Tommy F.
APPLICANT: NGUYEN, Duy-Viet An
APPLICANT: KLEEFELD, Yael
APPLICANT: GERSTIN, JR., Edward H.
APPLICANT: PERALTA, Careyna H.
APPLICANT: DAVID, Marie H.
APPLICANT: LEWIS, Samantha A.
APPLICANT: CHEN, Alice J.
APPLICANT: PANZER, Scott R.
APPLICANT: HARRIS, Bernard
APPLICANT: FLORES, Vincent
APPLICANT: MARWAHA, Rakesh
APPLICANT: LO, Audrey
APPLICANT: LAN, Ruth Y.
APPLICANT: URASHKA, Michael E.
TITLE OF INVENTION: MOLECULES FOR DISEASE DETECTION AND TREATMENT
FILE REFERENCE: PT-1231 PCT
CURRENT APPLICATION NUMBER: PCT/US02/09944
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: 60/280,067; 60/279,619; 60/291,280; 60/291,8
60/291,829; 60/299,428; 60/300,001; 60/299,776
PRIOR FILING DATE: 2001-03-29; 2001-03-28; 2001-03-29; 2001-05-16; 2001-05-17;
2001-05-17; 2001-06-19; 2001-06-20; 2001-06-20
NUMBER OF SEQ ID NOS: 792
SOFTWARE: PERL Program
SEQ ID NO 258
LENGTH: 6280
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
OTHER INFORMATION: Incyte ID No: LI:345320.4:2001MAY17
PCT-US02-09944-258

Query Match   93.9%; Score 1455.2; DB 1; Length 6280;
Best Local Similarity   97.6%; Pred. No. 1.4e-314;
Matches 1523; Conservative   0; Mismatches   28; Indels   10; Gaps   4;

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Qy      1 ATGGATGCTGACGAGGGTCAAGAGACATGTCTTTCCATCAGGAAGGAAGCCCCCCTGTA   60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    238 atggatgctgatgaggtcaagacagttccaagttcagggaaggaaagcccccctgta  297

Qy     61 A-GCGATACTCCAGATGAGGGCGATGAGCCCATGGCCATGCCGATCCCCGAGACCTCCACCAC  119
           | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    298 aggcgatactccagatgaggcgatgagcccatgccgatccccgagacctctccaccac  357

Qy    120 CTCGGGAGGACGCAGCAGCAAAGCTCCAAGAGTGACAGAGTCGTGGCCAGTAATGTTAAAGTAGA  179
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    358 ctcggggagacagcaagcaaagctccaagagtgacagagtcgtggccagtaatgttaaagtaga  417

Qy    180 GACTCAGAGTGATGAAGAAGAATGGGCGCTGCGTCTGTGAAATGAATGGGGAAGAATGTGCGGA  239
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    418 gactcagagtgatgaagaagaatgggcgctgcgtctgtgaaatgaatgggggaagaatgtgcgga  477

Qy    240 GGATTACGAATGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCCCACAGGGACCAAGG  299
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    478 ggattacgaatgcttgatgcctcgggagagagaaaatgaatggctcccacagggaccaagg  537

Qy    300 CAGCTCGGCTTTGTCGGGAGTTGGAGGCATTGCAGCTTCCTAACGGAAAACTAAAGTGTGA  359
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
Qy    601 CACAAATGTGGATATTGTGCGGCGAAGCTATAAACAGCAGCGTCTTTAGAGGAACATAAA  660
            ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db    769 cacaaatgtggatattgtggcgaagctataaacagcgaagctcttagaggaacataaa   828

Qy    661 GAGCGCTGCCACAACTACTTGAAAGCATGGGCCTTCCGGGCCACACTGTACCCAGTCATT   720
            |||||||||||||| ||||||||||||||||||||||||||||| |||||||||||||||
Db    829 gagcgctgccacaactacttggaaagcatgggccttccgggccacactgtacccagtcatt   888

Qy    721 AAAGAAGAAAACTAAGCACAGTGAAATGGCCAGAAGACCTGTGCAAGATAGGATCAGAGAGA   780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    889 aaagaagaaactaatcacagtgaaatggccagaagacctgtgcaagataggatcagagaga   948

Qy    781 TCTCTCGTGCTGGACAGACTAGCAAGTAAATGTCGCCAAACGTAAGAGCTTATGCCTCAG   840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    949 tctctcgtgctggacagactagcaagtaaacgtcgccaaacgtaagagctcctatgcctcag  1008

Qy    841 AAATTTCTTGGGGACAAGGGCCTGTCCGACACGCCCTACGA---CAGTGCCACCTACGAG   897
            ||||||||||| | |||| ||||| |||||||||||||||||      ||||||||||||
Db   1009 aaatttcttggggacaagggcctgtccgacacgcccagcagccgccagctacgag  1068

Qy    898 AAGGAGAACGAAAATGATGAAGTCCCACGTGATGACCAAGCCATCAACAACGCCATCAAC   957
            |||||||||||||||||||||||||||||||||||||||||||||||||||| ||| |
Db   1069 aaggagaacgaaaatgatgaagtcccacgtgatgaccaagccatcaacaacgccatcaac  1128

Qy    958 TACCTGGGGGCCGAGTCCCTGCCGCCCCCTGGTGCAGACGCCCCCGGGCCGGTTCCCAGGTG  1017
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1129 tacctgggggccgagtccctgccgcccccctgcgcccgccccgggccggttccgaggtg  1188

Qy   1018 GTCCCGGTCATCAGCCCGATGTACCAGCTGCACA---GGCGCTCGGAGGGCACCCCGCGC  1074
            ||||||||||||||||||||||||||||||||||    |||||||||||||||||||||
Db   1189 gtcccggtcatcagcccgatgtaccagctgcacaagcggcgctcgcggagggcaccccgcgc  1248

Qy   1075 TCCAACCACTCGGCCCAGGACAGCAGCGCCGTCGGACTACCTGCTCTCCAAGGCCAAG  1134
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1249 tccaaccactcggcccaggacagcgcgcctggagaacctgctgctctccaaggccaag  1308

Qy   1135 TTGGTGCCCTCGGAGCGCGGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACC  1194
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1309 ttggtgccctcggagcgcggcgggaggcgtccccgagcaacaagctgtcaagactccacggacacc  1368

Qy   1195 GAGAGCCAACAACGAGGAGCGCAGCGCTCCAGCCGGTCTTATCTACCTGACCAACCACATTCGCCCCG  1254
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1369 gagagcaacaacgaggagcgcagcgctccaggtctcatctacctgaccaaccacatcgccccg  1428

Qy   1255 CGGCGCC---AACGGCGTGTCGCTCAAGGAGGAGCCGCCTTACGACCTGCTGCCGGCGCC  1311
            ||||||    | | ||||||||||||||||||||||||||||||||||||||||||||||
Db   1429 cacgcgcgcaacggccttgtcgctcggagggcaccgcgcctacgacctgctgccgcgcc  1488

Qy   1312 GCCTTCCGAGAACTGCAGACGCGCCTCCGCGTGCTGGTCAGCACCAGCGGGGGAGCAGATGAAG  1371
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1489 gcctccgagaactgcgagacgcgctccgcgtgctggtcagcaccagcgggggagcagatgaag  1548

Qy   1372 GTGTACAAGTGCGAACACTGCCGCGGGTGCTCTTCCTGGATCACGTCATGTACACCATCCAC  1431
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1549 gtgtacaagtgcgaacactgccgcgggtgctctccttggatcacgtcatgtacaccatccac  1608

Qy   1432 ATGGGCTGCCACGCGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCACAGCCAG  1491
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1609 atgggctgccacgcgcttccgtgatcctttggagtgcaacatgtgcggctaccaccagccag  1668

Qy   1492 GACCGGTACGAGTTCTCGTCGCCACATAACCGCGAGGGGAGCACCCGCTTCCACATGAGCTAA  1551
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   1669 gaccggtacgagttctcgtcgcacataaccgcgagggggagcacccgcttccacatgagctaa  1728
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RESULT   4
PCT-US02-09944-258
; Sequence 258, Application PC/TUS0209944
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: DAFFO, Abel
; APPLICANT: JONES, Anissa L.

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Db   538 cagctcggcttttgtcgggagttggaggcattcgacttcctaacggaaactaaagtgtga 597

Qy   360 TATCTGTGGGATCATTTGCATCCGGCCCAATGTGCTCATGGTTCACAAAGAAGCCACAC 419
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   598 tatctgtgggatcatttgcatcggcgcccaatgtgctcatggttcacaaagaagcacac 657

Qy   420 TGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACCCAGAGGGCCAACCT 479
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   658 tggagaacggccccttccagtgcaatcagtgcgggggcctcattcacccagagggcaacct 717

Qy   480 GCTCCGGCACATCAAGCTGCATTCCGGGAGAGCCCTTCAAATGCCACCTGCAACTA 539
             |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   718 gctccggcacatcaagctgcattccgggagaagccccttcaaatgccaccctgcaacta 777

Qy   540 CGCCTGCCGCCGAGGCACGCCCTCACTGGCCACCTCCGTTGGTAAACC 599
             ||||||||||||||||||||||||||||||||||||||||||||||||
Db   778 cgcctgccgccgagggacgcccctcactggccacctccggttggtaaacc 837

Qy   600 TCACAAATGTGATATTTGTGGCCGAAGCTATAAACACGGAACGTCTTTAGAGGAACATAA 659
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   838 tcacaaatgtggatattgtggccgaagctataaacacggaacgtctttagaggaacataa 897

Qy   660 AGAGCGCTGCCACAACTACTTCGAAAGCATGGCCTTCGGGCACACTGTACCCAGTCAT 719
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   898 agagcgctgccacaactacttcgaaagcatggcctttcggggcacactgtacccagtcat 957

Qy   720 TAAAGAGAAACTAAGCACAGTGAAATGGCGAGAGAGCCTGTGCAAGATAGGATCAGAGAG 779
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   958 taaagagaaactaatcacagtgaaatggcgagagagcctgtgcaagataggatcagagag 1017

Qy   780 ATCTCGCTGCTGGACAGACTAGCAAGTAATGTGCCAAACTAAGAGTCTATGCCTCA 839
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1018 atctcgctgctggacagactagcaagtaacgtcgcaaacgtaagagctctatgcctca 1077

Qy   840 GAAATTTCTTGGGACAAGGGCCTGTCCGACACGCCCTACGA---CAGTGCCACGTACGA 896
             |||||||||||||||||||||||| ||| | | |||||  ||||
Db  1078 gaaatttcttgggacaaggggcctgtccgacacgcccctacgacagcgccagctacga 1137

Qy   897 GAAGGAGAACGAAATGATGAAGTCCCAGTGATGACCAAGCCATCAACAACGCCATCAA 956
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1138 gaaggagaacgaaatgatgaagtcccagtgatgaccaagccatcaacaacgccatcca 1197

Qy   957 CTACCTGGGGCCGAGTCCCTGCGCCCGCCCGTGTCGCAGAGCCGTTCCGAGGT 1016
             |||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db  1198 ctacctggggccgagtccctgcgcccgcccgtgtcgcagagccggttccggagt 1257

Qy  1017 GGTCCCGGTTCATCAGCCCGATGTACCAGCTGCACA---GGCGCTCGGAGGGCCACCCCGCG 1073
             ||||||||||||||||||||||||||||||||  |  | |||||||||||||||||||
Db  1258 ggtccccggttcatcagcccgatgtaccagcagcgcagcgctcggagggggcacccccgcg 1317

Qy  1074 CTCCAACCACTGGGCCCAGGACACGCGCCGTGGAGTACCTGCTCGCTCTCCAAGGCCAA 1133
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1318 ctccaaccactcggcccaggacacgcgccgtggagaacctgctgctctccaaggccaa 1377

Qy  1134 GTTGGTGCCCTCGGAGCGCGGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACAC 1193
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1378 gttggtgccctcggagcgcggaggcgtccccgagcaacagctgccaagactccacggacac 1437

Qy  1194 CGAGAGCAACAACGAGGAGGAGGCAGCGGAGGCGTCTTATCCTACCTGACCAACCACATCGCCCCG 1253
             ||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  1438 cgagagcaacaacgaggaggaggcagcggaggcgtctttatctgatcctgaccaaccacatcgccccg 1497

Qy  1254 ACGGCCGC---AACGGCGTGCTGCAGGAGGAGCAACGGGAGAACCTGCTGCGCGCGCG 1310
             | || | ||||||||||||||||||||||||| ||||||||||||||
Db  1498 gcacgcgcaacggcgcgcaacggcgtgctgctcaaggaggagcaacggctgctgcgcgcgcg 1557

Qy  1311 CGCCTCCGGAGAACTGCGACGCGCTCCGTGTGTGCAGCACCAGCGGGGAGCAGAATGAA 1370
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1558 cgcctccgagaactgcgacgcgctccgtgtgcagcaccagcgggggagcagaatgaa 1617

Qy  1371 GGTGTACAAGTGCGAACACTGCCGGGGGTGCTCTTCCTGGATCACGTCATGTACACCATCCA 1430
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1618 ggtgtacaagtgcgaacactgccgggggtgctctttcctggatcacgtcatgtacaccatccca 1677
```

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Qy  1431 CATGGGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACAATGTGCGCTACCACAGCCA 1490
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  1678 catgggctgccacgcttccgtgatcctttgagtgcaacatgtgcgctaccaccacagcca 1737

Qy  1491 GGACCGGTACGAGTTCTCGTCGCACATAACCGGAGGGGAGCGACCGCTTCCACATGAGCTA 1550
             ||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db  1738 ggaccggtacgagttctcgtcgcacataaccgagggggagcgacgtttccacatgagcta 1797

Qy  1551 A 1551
           |
Db  1798 a 1798
```

RESULT 5
US-08-733-622C-16
; Sequence 16, Application US/08733622C
; GENERAL INFORMATION:
;   APPLICANT: Georgopoulos, Katia
;   APPLICANT: Morgan, Bruce A.
;   TITLE OF INVENTION: AIOLOS GENE
;   FILE REFERENCE: 10287-030001
;   CURRENT APPLICATION NUMBER: US/08/733,622C
;   CURRENT FILING DATE: 1996-10-17
;   PRIOR APPLICATION NUMBER: US 60/017,646
;   PRIOR FILING DATE: 1996-05-14
;   PRIOR APPLICATION NUMBER: US 60/005,529
;   PRIOR FILING DATE: 1995-10-18
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: FastSEQ for Windows Version 4.0
;
; SEQ ID NO 16
;   LENGTH: 1386
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(1383)
US-08-733-622C-16

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Query Match             89.4%;  Score 1386;  DB 4;  Length 1386;
Best Local Similarity  100.0%;  Pred. No. 7e-299;
Matches 1386;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   166 AATGTTAAAGTAGAGACTCAGAGTGATGAAGAGAATGGGCGCTGCCTGTGAAATGAATGGG 225
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     1 aatgttaaagtagagactcagagtgatgaagagaatgggcgctgtgaaatgaatgggg 60

Qy   226 GAAGAATGTGCGGAGGATTTACGAATGCTTGATGCCTCGGGAGAGAAAATGAATGGCTCC 285
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    61 gaagaatgtgcgggaggatttacgaatgcttgatgcctcgggagagaaaatgaatggctcc 120

Qy   286 CACAGGGACCAAGGCAGCAGCTCGGCTTGTCGCGGAGTTGGAGGCATTCGACTTCCTAACGGA 345
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   121 cacagggaccaaggcagcagctcggcttgtcggggagttggaggcattcgacttcctaacgga 180

Qy   346 AAACTAAAGTGTGATATCTGTGGGGATCATTTGCATCGGCGCCCAATGTGCTCATGGTTCAC 405
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   181 aaactaaagtgtgatatctgtgggggatcatttgcatcggcgcccaatgtgctcatggttcac 240

Qy   406 AAAAGAAGCCACACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACC 465
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   241 aaaagaagccacactggagaacggcccttccagtgcaatcagtgcgggggcctcattcacc 300

Qy   466 CAGAGGGCAACCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAGCCCTTCAAATGC 525
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   301 cagaagggcaacctgctccggcacatcaagctgcattccggggagaagccctcaaatgc 360

Qy   526 CACCTCTGCAACTACGCCTGCCGCCCGGAGGACGCCCTCACTGGCCACCTGGAGGACCAC 585
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   361 caccctgcaactacgcctgccgcccggaggacgccctcactggccacctggaggacgcac 420

Qy   586 TCCGTTGGTAAACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACACGGAACGTCT 645
```

```
;   APPLICANT: Morgan, Bruce A.
;   TITLE OF INVENTION: AIOLOS GENE
;   FILE REFERENCE: 10287-030001
;   CURRENT APPLICATION NUMBER: US/08/733,622C
;   CURRENT FILING DATE: 1996-10-17
;   PRIOR APPLICATION NUMBER: US 60/017,646
;   PRIOR FILING DATE: 1996-05-14
;   PRIOR APPLICATION NUMBER: US 60/005,529
;   PRIOR FILING DATE: 1995-10-18
;   NUMBER OF SEQ ID NOS: 38
;   SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 18
;   LENGTH: 2049
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (223)...(1776)
US-08-733-622C-18
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Query Match             75.7%;  Score 1174.8;  DB 4;  Length 2049;
Best Local Similarity   87.2%;  Pred. No. 7e-252;
Matches 1365;  Conservative   0;  Mismatches 177;  Indels   24;  Gaps   6;

Qy      1 ATGGATGCTGACGAGGTCAAGACACATGTCTTTCTCATCAGGAGGAAAGCCCCCTGTA 60
          |||||||| |||||| ||| |||| | ||| |||||  |||||||| |||||||||| |
Db    223 atggatgtcgatgaggtcaagacagtccaagttcaggaaaggagagcccccccagtc 282

Qy     61 AGCGATACTCCAGATGAGGGCGATGAGCCCATGGCCCATGGGGAGGACCTCTCCACCACC 120
          || || |||||| | |||||||| |||| ||| |||||||| ||||| ||||||| |||
Db    283 agtgacactccagatgaagggatgagcccatgcagggccagtcctgaggacctgccactacc 342

Qy    121 TCGGGAGGACAGCAAAGCTCCAAGAGTGACAGAGTTCGTGGCCAGTAATGTTAAAGTAGAG 180
          |||||| | ||||| || |||||||| |||||| ||||||||| |||||| |||||||||
Db    343 tctggagcacagcagactccaagaggtgatcgaggcatggcagtcagtaatgttaaagtagag 402

Qy    181 ACTCAGTGATGATGAAGAGAATGGGCGTGCCTGTGAAATGAATGGGGAAGAAATGTCGGAG 240
          ||| |||||| || ||||||||||||||| |||| || |||  |||||||||| |||||||
Db    403 actcagtgatgatgaagaatgggcgtgcctgtgaaatgaatgggaagaaatgtcgcagag 462

Qy    241 GATTTACGAGTCTTGATGCCTCGGGAGAGAAATGAATGGCTCCCACAGGGACCAAGGC 300
          || | ||||| ||| || | | |||||| |||| || ||| ||||| ||||||| |||
Db    463 gatttacgaatgtttgatgcctgtcggggagaaatgaatgtctcccacagggaccaaggc 522

Qy    301 AGTCCGGCTTGTCGGGAGTTGGAGCATTCGACTTCTTAACGGAAAACTAAAGTGTGAT 360
          ||||| |||| || |||| || || |||||||| ||| ||||||||| ||||| |||||
Db    523 agtccggctttgtcgggagttggaggcattcgagactcctaacgagaaaactaaagtgtgat 582

Qy    361 ATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTGGGGGCCTCATTCACCCAGGGAGCAG 420
          ||| ||||| |||| |||||||||||||||||||| |||| ||||| |||| ||| |||||
Db    583 atctgtgggatcgttcatgtggcatcggcccaatgtgctcatgtttcacaaaagaagtcatact 642

Qy    421 GGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACCCAGAGGGCAACCTG 480
          || || ||||| |||||| |||||| |||||||||||||| ||| ||||| ||||| ||
Db    643 ggtgaacggccttccagtgcaaccagtctgggccctccttcacccagaaagcaacctc 702

Qy    481 CTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCTCTGCAACTAC 540
          |||| ||||| |||| || |||| ||||||||| ||||| ||||| |||||| ||||| ||
Db    703 ctgcggcacatcaagctgcactcggtgagaagccctcatcttgcaactat 762

Qy    541 GGCTGCCGCCGGAGGGACGCCCTCACTGGCCACCGCCACTCCGTTGGTAAACCT 600
          |||||||| ||||| ||| ||||| ||| ||||| || |||||| |||||| ||
Db    763 ggctgccgccgagggacgccctcaccggccaccctgagggtaagcct 822

Qy    601 CACAAATGTGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGAGGAACATAAA 660
          ||||||||||| | ||||| ||||| || |||| |||||| | ||||  |||||||
Db    823 cacaaatgtggatattgttggccggagctaaacagcggatcttttagaggagcataaa 882

Qy    661 GAGCGGCTTGCCACAACTACTTGGAAAGCCATAGCGGCCTTCCGGGCACACTGTACCCAGTTCATT 720
          |||| |||||||||||||| |||||| ||||| |||||||||||||||||||||
Db    883 gagcggatgccacaactacttggaaagcatgggcctccgggc---ggtgccagtcatt 939
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```
Db    421 tccgttggtaaacctcacaaatgtggatattgtggccgaagctataaacagcgaacgtct 480
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    646 TTAGAGGAACATAAAGCAGCGGCTTGCCACAACTACTTGGAAAGCCATAGCGGCCTTCCGGGCACACA 705
          ||||||||||||||||||||||||||||||||||||||
Db    481 ttagaggaacataaagcgctggacactactcgaaagcatggggcacaca 540
```

```
Qy    706 CTGTACCCAGTCATTAAGAGAAGAAACTAAGCACACGTGAAATGGCAGAAGACCTGTGCAAG 765
          |||||||||||||||||||||||||||||||||||||||||||
Db    541 ctgtaccagtcattaagagaaaaactaagcacagtgaaatggcagaagacctgtgcaag 600
```

```
Qy    766 ATAGGATCAGAGAGATCTCTCGTGCTTGGACAGACTAGCAAGTAATGTCGCCAAACGTAAG 825
          |||||||||||||||||||||||||||||||||||||||||
Db    601 ataggatcagagagagatctctcgtgctggacagactagcaagtaatgtcgccaaacgtaag 660
```

```
Qy    826 AGCTCTATGCCTCAGAAATTCTTGGGACAAGGGCCTGTCCGACAACGCCCTACCACAGT 885
          ||||||||||||||||||||||||||||||||||||||||||||
Db    661 agctctatgcctcagaaattcttgggacaagggcctgtccgacacgccctaccacagt 720
```

```
Qy    886 GCCAGTACGACGAGAAGGAGAACGAAATGATGAAGTCCACGTGATGACCAAGCCATCAAC 945
          ||||||||||||||||||||||||||||||||||||||||||||||
Db    721 gccagtacgacgagaaggagaacgaaatgatgaagtccacgtgatgaccaagccatcaac 780
```

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Qy    946 AACGCCATCAACTACCTGGGGCGACTCCCTGCGCCTGGTGCAGACGCCCCCGGGC 1005
          ||||||||||||||||||||||||||||||||||||||||
Db    781 aacgccatcaactacctggggcgactcccgtgcgccggtgcagacgcccccgggc 840
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Qy   1006 GGTTCCGAGGTGTCCGGTCATCAGCCGGATGTACCAGCTGCACAGGCGCTCGGAGGGC 1065
          ||||||||||||||||||||||||||||||||||||||||
Db    841 ggttcgagggtggtcccggtcatcagccgggctacagcgctcgggaggggc 900
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```
Qy   1066 ACCCGGCGCTCCAACCACTCGGCCACCGGACGCGGCCTGGAGTACCTGCTGCTCTCC 1125
          ||||||||||||||||||||||||||||||||||||||||
Db    901 acccggcgctccaaccactcggccaccgcgggcctggagtacctgctgctctcc 960
```

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Qy   1126 AAGGCCAAGTTGTGCCCTCGGACGCGCGAGCGTCCCCGGCCAACAGCTGCCAAGACTCC 1185
          ||||||||||||||||||||||||||||||||||||||||
Db    961 aaggccaagttggtgccctcggacgcgagcgtccccgagcaacagctgccaagacctcc 1020
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Qy   1186 ACGGACACCGAGACAACAACGAGCAGCGGCAGCGGTCTTTATCCTACCTGACCAACCAC 1245
          ||||||||||||||||||||||||||||||||||||||||
Db   1021 acggacaccgagagacaacgagcagcgccagcgtctctatctacctgaccaaccac 1080
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Qy   1246 ATCGCCCGACGCGCGCAACGCGTGTCGCTCAAGGACAGCGCCGCCTACGACACCGCTGCTG 1305
          ||||||||||||||||||||||||||||||||||||||||
Db   1081 atcgcccgacgcgcgcaacgcgtgtcgctcaaggaggagcaccgcgcctacgacacctgctg 1140
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Qy   1306 CGGCCGCCTCCGAGAACTCGCGAGACGCGCTCCGCGTGGTCAGCAGCGGGGAGCAG 1365
          ||||||||||||||||||||||||||||||||||||||||
Db   1141 cggccgccgctccgagaactcgcgagacgcgctccgcgtggtcagcagcggggagcag 1200
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Qy   1366 ATGAAGGTGTACAAGTGCGAACACTGCCGAACACTGCCGGATCACGTCATGTACACC 1425
          ||||||||||||||||||||||||||||||||||||||||
Db   1201 atgaaggtgtacaagtgcgaacactgccgggtgtctcttcctgatcacgtcatgtacacc 1260
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Qy   1426 ATCCACATGGCTGCCACGGCTTCCACGGCTTGCACCGTGATCACTCTTCTTGAGTGCAACATGTGCGGCTACCAC 1485
          ||||||||||||||||||||||||||||||||||||||||
Db   1261 atccacatggctgccacggcttccacggcttgcacatgtgatcatctttgagtgcaacatgtgcggctaccac 1320
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Qy   1486 AGCCAGGACCGGTACGAGTTCTCGTCGCACATAACGCCGAGGGGAGCACCGCTTCCACATG 1545
          ||||||||||||||||||||||||||||||||||||||||
Db   1321 agccaggaccggtacgagttctcgtcgcacataacgccgaggggagcaccgcttccacatg 1380
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Qy   1546 AGCTAA 1551
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Db   1381 agctaa 1386
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RESULT   6
US-08-733-622C-18
;   Sequence 18, Application US/08733622C
; GENERAL INFORMATION:
;   APPLICANT: Georgopoulos, Katia
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Query Match     56.0%;     Score 868;   DB 4;   Length 1004;
Best Local Similarity   88.8%;     Pred. NO. 1.1e-183;
Matches 1004;   Conservative   0;   Mismatches   0;   Indels 126;   Gaps   0;

Qy  421 GGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGCGCCTCATTCACCCAGAAGGGCAACCTG 480
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    1 ggagaacggcccttccagtgcaatcagtgcgggcgcctcattcacccagaagggcaacctg 60

Qy  481 CTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCTCTGCAACTAC 540
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 ctccggcacatcaagctgcattccggggagaagcccttcaaatgccacctctgcaactac 120

Qy  541 GCCTGCGCCGGAGGGACGACCCCTCACTGGCCACCTGGCACCTCCGTTGGTAAACCT 600
         |||||||||||||||||||||||||||||||||||||||||
Db  121 gcctgcgccggagggacgcccctcactggccacctggccacctcc------------ 168

Qy  601 CACAAATGTGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGAGGAACATAAA 660
Db  169 --------------------------------------------------------- 168

Qy  661 GAGCGCTGCCACAACTACTTGGAAAGCATGGCCGCCTTCCGGGCACACACTGTACCCAGTTCATT 720
                                                                      ||||||
Db  169 -------------------------------------------------gtcatt 174

Qy  721 AAAGAAGAACTAAGCACAGTGAAATGCGAAGATAGGATCAGAGAGA 780
         ||||||||||||||||||||||||||||||||||||||||||||||
Db  175 aaagaagaaactaagcacagtgaaatgcgaagataggatcagagaga 234

Qy  781 TCTCTCGTGCTGGACAGACTAGCACAGCTAAGTCGCCAAACGTAAGAGCTCTATGCCTCAG 840
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  235 tctctcgtgctggacagactagcacagctaagtcgccaaacgtaagagctctatgcctcag 294

Qy  841 AAATTTCTTGGGGACAAGGGCCTGTCCGACACGCACGCCCTACGACTGCCACGTACGAGAAG 900
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  295 aaatttcttggggacaaggggcctgtccgacacgcacgccctacgactgccacgtacgagaag 354

Qy  901 GAGAACGAAATGATGAAGTCCCACGTGATGGACCATCAACAACGCCATCAACTAC 960
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Db  355 gagaacgaaatgatgaagtcccacgtgatggaccatcaacaacgccatcaactac 414

Qy  961 CTGGGGGCCGAGTCCCTGCGCCCGTTCCGAGGTGGTC 1020
         |||||||||||||||||||||||||||||||||||||
Db  415 ctgggggccgagtccctgcgcccgttccgaggtggtc 474

Qy 1021 CCGGTCATCAGCCGATGTACCAGCTGCACAGGCCGCTCGGAGGGCCGCTCCAAC 1080
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  475 ccggtcatcagccgatgtaccagctgcacaggccgctcggagggccgctccaac 534

Qy 1081 CACTCGGCCCAGGACAGCGGCCGTGGAGTACCTGCTCTCCAAGGCCAAGTTGGTG 1140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  535 cactcggcccaggacagcggccgtggagtacctgctctccaaggccaagttggtg 594

Qy 1141 CCCTCGAGCGCGGAGGGGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAGAGC 1200
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  595 ccctcgagcgcggaggggtccccgagcaacagctgccaagactccacggacaccgagagc 654

Qy 1201 AACAACGAGGAGGCCCAGCCGGTCTTATCTACCTGACCAACATCACCGCCCGACCGCCG 1260
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  655 aacaacgaggaggcccagccggtcttatctacctgaccaacatcaccgcccgaccgcgcg 714
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Qy  721 AAAGAAGAACTAAGCACAGTGAAATGCGAGAGAACCTGTGCAAGATAGGATCAGAGAGA 780
         ||  ||||||||||  |||   |  ||  ||||   ||||||||||||||  |||||||
Db  940 aggaagaaactaaccaccacgagatggcagaagatggcagaagacctgtgcaagataggagcagagagg 999

Qy  781 TCTCTCGTGCTGGACAGACTAGCACAGCTAAGTCGCCAAACGTAAGAGCTCTATGCCTCAG 840
         ||  ||  ||| || ||  ||  |  ||  || || |||||||||||||||||||||||||
Db 1000 tccttgtcctggacaggctggcaagcaatgtcgccaaacgtaagagctaagagctctatgcctcag 1059

Qy  841 AAATTTCTTGGGGACAAGGGCCTGTCCGACACGCCCTACGACTGCCACGTACGAGAAG 900
         |||||||||| |||||||  |||||| ||||||| ||||   ||||  |||||||||
Db 1060 aaatttcttggagacaagtgcctgtcagacatgcgccatatgacaatatgaagaag 1119

Qy  901 GAGAACGAAATGATGAAGTCCCACGTGATGGACCATCAACAACGCCATCAACTAC 960
         |||      |||||||||||||||||||||| ||||||||| |||||||||||||
Db 1120 gag--gatatgatgacatcccacgtgatgatcaacaatgccatcaactac 1176

Qy  961 CTGGGGGCCGAGTCCCTGCGCCCGTTCCGAGGTGGTC 1020
         ||||||| | ||  | || | | ||  | || || ||
Db 1177 ctgggggctgagtgagtcccgtgcgcgccattgtgcagacaccccggtagctccgagttggtg 1236

Qy 1021 CCGGTCATCAGCCGATGTACCAGCTGCACAGG 1077
         |||||||||||| |||||||||||||||||
Db 1237 ccgtcatcagctccatgtaccagctgcacacagg 1296

Qy 1078 AACCACTCGGCCCAGGACAGCGGCCCGTGGAGTACCTGCTCTCTTCCAAGGCCAAGTTG 1137
         |||||||||||||||  | ||||||  |||||||||||||   |||||||||||||||
Db 1297 aaccattcagcacagga---cgccgtggataacttgctgctgtgtgtccaagccaagtct 1353

Qy 1138 GTGCCCTCGAGCGCGGAGGGGTCCCCGAGCAACTGCCACCCGAG 1197
         |||||||||||||||||| |||||   |  |||
Db 1354 gtgtcatcggagcgagaggcctcccgacaacagcgtgccaagactccagatacagag 1413

Qy 1198 AGCAACAACGAGGAGGCAGCGCAGCCGGTCTTATCTACCTGACCAACCATCCCCGACGC 1257
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Db 1414 agcaacgcggaggaacagcgcagccgcggccttatctacctaaccaaccaaccatcaacccgcat 1473

Qy 1258 GCGC--AACGGCTGTGCCTCAAGGAGAGCACCGCCTACGACCTGCCTGCGCGGCCGCC 1314
         |||   ||  |||| | ||  |||||||| |||||| || |  |||| || || | ||
Db 1474 gcacgcaatgggctggcctcaggaggagcaccggctgcgaggtgtgctgaggtgcggcc 1533

Qy 1315 TCCGAGAACTCGCAGGACGCGGCTCGGCTGCGTGTCAGCACAGGGGGGAGCAGCAGTGAAGGTG 1374
         || ||||||||  | || |||||  |||  |  |||  ||  |||||||||||| ||||||
Db 1534 tcagagaactgcaggatgcctccgtgtggtcagcagcagctggcgagctgaaggtg 1593

Qy 1375 TACAAGTGCGAACACTGCCGGGTGTCTCTTCTCTGATCACGTCATGTACACCATCCACATG 1434
         ||||| ||||  |||||||||| | || |  | ||||| |||| ||| ||||||||||
Db 1594 tacaagtgcgaaacactgccgggtgctccggatcacgtctcatgtataccattcacatg 1653

Qy 1435 --------GGCTGCCACGGCTTCCGGTGATCGCTTTTGAGTGCAACATGTGCGGCTACCAC 1485
                 || |||| ||| || | ||||| |||||| |  | |||||| | | ||||||||
Db 1654 ggctgccatggctgccatggatcccttgagtgtaacatgtgttattac 1713

Qy 1486 AGCCAGGACCACCGGTACGAGTTCTCGTGCCACATAACGCGGAGCACCGCTTCCACATG 1545
         |||||| |||||||||  |||||| || |||||| || |||||||| ||| || ||||
Db 1714 agccaggacagtggtacgagttcatcatcccataccacgcgggggggccatcgttaccacctg 1773

Qy 1546 AGCTAA 1551
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Db 1774 agctaa 1779
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Qy  1261 CAACGCGGTGTCGCTCGCTCAAGGAGGAGCACCGCCGCCTGCTGCGCGCCTCCGAG 1320
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Db   715 caacgcgtgtcgctcaaggaggagcaccgccgcctacgacctgctgcgcgccctccgag 774

Qy  1321 AACTCGCAGGACGCCGCTCCGCGTGGTCAGCAGATGAAGCGGGGAGCAGATGTACAAG 1380
         |||||||||||| |||||||||||  |||||||||||||||||||||||||||||
Db   775 aactcgcaggacgcgctccgcgtcggtcagcaccagcgggagcagatgaaggtgtacaag 834

Qy  1381 TCGGAACACTGCCGGGTGCTCTTCCTGGATCACGTGCTCATGTACACCATCCACATGGCTGC 1440
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Db   835 tgcgaacactgccgggtgctcttcctggatcacgtcatgtacaccatccacatgggctgc 894

Qy  1441 CACGGCTTCCGTGATCCTTTGAGTGCAACATGCCGCTACCAGCCCAGGACCCGTAC 1500
         ||||||||||||||||||||||||||||||| || |||||||||| ||||||||||
Db   895 cacggcttccgtgatccttttgagtgcaacaatgtgcggctaccacacccagggacccgtac 954

Qy  1501 GAGTTCTGTCGCACATAACGCGAGGGGAGCACCGCCTTCCACATGAGCTA 1550
         |||||| ||||||||||||||||||| ||||||||||||||||||||||
Db   955 gagttctcgtgtcgcacataacgcgagggggagcaccgccttccacatgagcta 1004


RESULT  8
US-10-035-832-1159
; Sequence 1159, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 1613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1159
; LENGTH: 1296
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-035-832-1159

Query Match       52.5%;  Score 814.8;  DB 6;  Length 1296;
Best Local Similarity   85.6%;  Pred. No. 8e-172;
Matches   984;  Conservative   0;  Mismatches 142;  Indels  24;  Gaps  6;

Qy   417 CACTGGAGAACGGCCCTTCCAGTGCGGGCCTCAATCAGTGCGGGCCTCATTCACCCAGAAGGGCAA 476
         || || ||||||||||||||||||   ||||||||||| || |||||| ||||||||||
Db   156 catgggtgaacggcccttccagtgcaaccagtgtgggccttaccccagaaaggcaa 215

Qy   477 CCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCTGCAA 536
         || |||||||||||||||||||||| ||| ||||||||||||| |||||||||||
Db   216 cctcctgcggcacatcaagctgcactcggg tgggtgagaagcccatcttgcaa 275

Qy   537 CTACGCCTGCCCCCGGAGGACGCGCCCTCACTGGCCACCTCCGTTGGTAA 596
         ||| |||| ||||||| ||  ||||| |||||| ||||| |||||||
Db   276 ctatgcctgcccggagggacgccctcaccctgaggacgcactccgttggtaa 335

Qy   597 ACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGGAGGAACA 656
         |||||| ||||| |||||| ||||| || ||||| || |||| |||||| |||||||||
Db   336 gcctcacaaatgtggatattggcgccggagcctataaacagcgaactctttagaggagca 395

Qy   657 TAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCACACTGTACCAGT 716
         |||||||| |||||||||||||||||||||||||||||||||||| || ||||||
Db   396 taaagagcgatgccacaactacttggaaagcatgggccttccgggc--gtgtgcccagt 452

Qy   717 CATTAAAGAAGAGAAACTAAGCACAGTGAAATGCCAGAAGACCTGTGCAAGATAGGATCAGA 776
         |||||||||||||||| |||||| ||| ||||||| |||| ||||||||||||||||||
Db   453 cattaaggaagagaaactaaccaacaacagatggcagagaccctgtgcaagataggagcaga 512
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Qy   777 GAGATCTTCGTGCTGGACAGACTAGCAAGCTAGCAAGTAATGCTGCCAAAGCTAAGAGCTCTATGCC 836
         ||| ||  ||  || |||| ||||| |||||||  ||||||||  |||||||||||
Db   513 gaggtccctgtcctgacaggctggcaagcaatgtcaagcaatgtcatgcc 572

Qy   837 TCAGAAATTCTTGGGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGA 896
         |||||||| |||  |||| || |||||  ||| || |||||||||||||||  ||||
Db   573 tcagaaatcttggacaagtgcctgtcagacatgccctatgacagtgccaactatga 632

Qy   897 GAAGGAGAACGAAAATGATGAAGTCCACGTGATGACCAAGCCATCAACAACGCCATCAA 956
         |||||||   |||| || ||   |||||||||| |||| ||||||||||| ||||||||
Db   633 gaaggag---gatatgatgacatcccacgtgatggaccaggccatcaacaatgccatcaa 689

Qy   957 CTACCTGGGGGCGAGTCCCTGCGCCCCCTGGTGCAGACGCCCCCGGCGGGTTCCGAGGT 1016
         |||||||||| | ||||| ||||||||  |||||| |  | |||||  ||| ||||||
Db   690 ctacctggggctgagtcccctgcgccccatggtgcgacaccccgtagtccgaggt 749

Qy  1017 GGTCCCGGTCATCAGCCCGATGTACCAGCTGCACAGGCG---CTCGGAGGGCACCCGCG 1073
         ||| ||||||||||||  ||||   |||| |||| || |    | |||||||||| | |
Db   750 ggtgccagtcatcagctccagtgcaaagcccccctcagatggccccccacg 809

Qy  1074 CTCCAACACTCGGCCCAGGACGACAGCGCCGTGGAGTACCTCTGCTCCTCCAAGGCCAA 1133
         |||||| ||| ||| ||||| ||||||||| |  | ||| ||||| |  |||||||||
Db   810 gtccaaccattcagcacagga--cgccgtggataacttgctgctcgtgctcgtccaaggccaa 866

Qy  1134 GTTGGTGCCCTCGGAGCGCGCAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACAC 1193
         |  |||| | |||||||| |  |||| ||||| |||||||||||||||||| ||| | ||
Db   867 gtctgtgtcatcggagcggagggcctcccccagcaacagctgccaagaccccacagatac 926

Qy  1194 CGAGAGCAACAACAGGAGGAGGAGCCAGCGGTCTTATCTACCTGACCAACCACACATCGCCCCG 1253
         ||||||||||  ||| || |  | |||| || |||||||||||  |||| |||| |  |||| 
Db   927 agagagcaacgcggaggaacagcgcagcggcccttatctacctaaccaaccacatcaaccc 986

Qy  1254 ACGCGCGC---AACGCGTGTCGCTCAAGGAGGAGCACCGCCTACGACCTGCTCGCGC 1310
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Db   987 gcatgcacgcaatgggctgtctcaaggagagcaacgcgccctacgaggtgctgaggggc 1046

Qy  1311 CGCCTCCGAGAACTCGCAGGACGGCGTCCGCGTGTCAGCACCACCAGCGGGGAGCAGATGAA 1370
         ||||||  ||||||||||||| |  ||||  |||||||  |   || |||  ||||| |||
Db  1047 ggcctcagagagaactcgcaggatgcctccgtggtgtcagcgagtggcgagcagctgaa 1106

Qy  1371 GGTGTACAAGTGCGAACACTGCCGGGTGCTCTTCCTGGATCACGTGCTCATGTACACCATCCA 1430
         |||||||||||||||||||||||| ||||||||||||||||||||||||||||| |||||| |
Db  1107 ggtgtacaagtgcgaacactgccgcgtgctcttcctggatcacgtgctcatgtataccattca 1166

Qy  1431 CATG--------GGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTA 1481
         ||||        ||||||||  ||| |||| ||||||| |||| |||||||| | | ||
Db  1167 catgggctgccatggctcgccatgtcggatccctttgagttgtaacatgtgtggtta 1226

Qy  1482 CCACAGCCAGGACCCGGTACGAGTTCTCGCGTCGCACATAACCGGGGAGCACCGCCTTCCA 1541
         |||||||||||||  |||||||||||||   |  |||||  ||| ||||||| |||| ||
Db  1227 tcacagccaggacaggtacgagttctcatcccatatcacgcggggggggagcatcgttacca 1286

Qy  1542 CATGAGCTAA 1551
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Db  1287 cctgagctaa 1296


RESULT  9
US-09-053-375B-942
; Sequence 942, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chenchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 942
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Mus musculus
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US-09-053-375B-942

Query Match   52.5%;   Score 814.8;   DB 5;   Length 1550;
Best Local Similarity   85.6%;   Pred. No. 8.1e-172;
Matches 984;   Conservative   0;   Mismatches 142;   Indels 24;   Gaps   6;

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Qy   417 CACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACCCAGAAGGGCAA 476
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Db   194 catgggtgaacggccctttccagtgcaacaagtggggcctccttttacccagaaggcaa 253

Qy   477 CCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCTCTGCAA 536
         ||| ||| |||||||||||| || |||| ||||||||||| ||||| |||||||| ||||
Db   254 cctcctgcggcacatcaagctgcactcggggtgagaagcccttcaaatgccatctttgcaa 313

Qy   537 CTACGCCTGCCGCCGGAGGACGGCCCCTCACTGGCCACTGGATGACGCGCCACTCCGTTGGTAA 596
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Db   314 ctatgcctgccgccgggaggacgccctcaccggccactggatgacgcgccactccgttggtaa 373

Qy   597 ACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGGCAACGCTCTTTAGAGGAACA 656
         |||||||||||||||||||| |||||| |||||||||| |||||||||||||||||| |||
Db   374 gcctcacaaatgtggatattgtggccggagctataaacagcgaagctctttagaggagca 433

Qy   657 TAAAGAGCGCTGCCAACTACTTGGAAAGCATGGGCCTTCCGGGCCACACTGTACCCAGT 716
         |||||||| |||||| |||||||||||||||||||||||||||||   || |||||||
Db   434 taaagagcgatgccaacaactacttggaaagcatgggccttccgggc---gtgtgcccagt 490

Qy   717 CATTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGACCTGTGCAAGATAGGATCAGA 776
         ||||||| ||||||||||||||||||||||||||||||    || |||||||||| ||||
Db   491 cattaaggaagaaactaagcacagtgaaatggcagaaggtggcaagataggagcaga 550

Qy   777 GAGATCTCTCGTGCTGGACAGACTAGCAAGTAATGTCCCAAACGTAAGAGCTCTATGCC 836
         ||||| || |||||||||||| || |||||||| || || ||||||||||||||||||
Db   551 gaggtccctgtcctggacagctggcaagcaatgtcgcaaacgtaagagctctatgcc 610

Qy   837 TCAGAAATTTCTTGGGGACAACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGA 896
         |||||||||||||| |||||   |||||||| ||||| || |||||| |||||||||| ||
Db   611 tcagaaatttcttggagacaagtgcctgtcagacagtgccaactatga 670

Qy   897 GAAGGAGAACGAAATGATGAGTGAGTCCCACGTGATGGACCAAGCCATCAACAACGCCATCAA 956
         |||||| || |||||| || |||| |||||| |||||||||||||||||||||||||||||
Db   671 gaaggag---gatatgatgacatcccacgtgatggaccaggccatcaacaacgccatcaa 727

Qy   957 CTACCTGGGGGCCCAGTCCCTGCCGCCCCGGCCGTTCCGAGGT 1016
         |||||| |||||| ||||||||| ||||||||||| |  |||||
Db   728 ctacctggggggctgagtccctgcgccattggtgcagcaccccccggtagctccgaggt 787

Qy  1017 GGTCCCGGTCATCAGCCCCGATGTACCAGCTGCACAGGCG---CTCGGAGGGCACCCCGCCG 1073
         ||  |||||| |||||  ||   ||| |||| ||||||||    ||  ||||||||  ||||
Db   788 ggtgccagtcatcagctccatgtaccagctgccaaggtggccccccacg 847

Qy  1074 CTCCAAACCACTCGGCCCAGGAGGCGCCCCAGGAGTACCTGCTTCCTCAAGGCCAA 1133
         |||||||||||||||| || |||| |||||||| |||||| |  ||||||||||||
Db   848 gtccaaccattcagcacgga---cgccgtggataacttgctgctgctgtccaaggccaa 904

Qy  1134 GTTGGTGCCCTCGAGCGGCCGAGCGTCCCGAGCAACAGCTGCCGAAGACTCCACGGACAC 1193
         |  ||| |||||||||| || ||||| |||||||||||||||| || |||||||||||||
Db   905 gtctgtgtcatggagcgagaggcctcccccgagcaactacttggagacactccacgga---
```

RESULT 10
US-10-035-832-1158
; Sequence 1158, Application US/10035832
; GENERAL INFORMATION:
; APPLICANT: Morris, David
; APPLICANT: Engelhard, Eric
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
; FILE REFERENCE: A-71249/RMS/DCF
; CURRENT APPLICATION NUMBER: US/10/035,832
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; SOFTWARE: PatentIn version 3.1
; NUMBER OF SEQ ID NOS: 1613
; SEQ ID NO 1158
; LENGTH: 1550
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-035-832-1158

Query Match   52.5%;   Score 814.8;   DB 6;   Length 1550;
Best Local Similarity   85.6%;   Pred. No. 8.1e-172;
Matches 984;   Conservative   0;   Mismatches 142;   Indels 24;   Gaps   6;

```
Qy   417 CACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGGCCTCATTCACCCAGAAGGGCAA 476
         |||||| |||||||||||||| |||| |||||| ||||| |||||| || ||||||||||
Db   194 catgggtgaacggccctttccagtgcaacaagtggggcctccttttacccagaaggcaa 253

Qy   477 CCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCTCTGCAA 536
         ||| ||| |||||||||||| || |||| ||||||||||| ||||| |||||||| ||||
Db   254 cctcctgcggcacatcaagctgcactcggggtgagaagcccttcaaatgccatctttgcaa 313

Qy   537 CTACGCCTGCCGCCGGAGGACGGCCCCTCACTGGCCACTGGATGACGCGCCACTCCGTTGGTAA 596
         |||| |||||||||||| |||||| |||||| |||||||||||||||||||||| |||||||||
Db   314 ctatgcctgccgccgggaggacgccctcaccggccactggatgacgcgccactccgttggtaa 373

Qy   597 ACCTCACAAATGGATATTGTGGCCGAAGCTATAAACAGGCAACGCTCTTTAGAGGAACA 656
         |||||||||||  ||||||||||| ||| ||||||||| |||| || ||||||||||| |||
Db   374 gcctcacaaatgtggatattggggtcgcgagctataaacagcgaagctcttttagaggagca 433

Qy   657 TAAAGAGCGCTGCCAACTACTTGGAAAGCATGGGCCTTCCGGGCCACACTGTACCCAGT 716
         |||||||| |||||| |||||||||||||||||||||||||||||   || |||||||
Db   434 taaagagcgatgccaacaactacttggaaagcatgggccttccgggc---gtgtgcccagt 490

Qy   717 CATTAAAGAAGAAACTAAGCACAGTGAAATGGCAGAAGACCTGTGCAAGATAGGATCAGA 776
         ||||||| ||||||||||||||||||||||||||||||    || |||||||||| ||||
Db   491 cattaaggaagaaactaagcacagtgaaatggcagaaggtggcaagataggagcaga 550

Qy   777 GAGATCTCTCGTGCTGGACAGACTAGCAAGTAATGTCGCAAAACTAAGAGCTCTATGCC 836
         ||||| || |||||||||||| || |||||||| || || |||  |||||||||||||
Db   551 gaggtccctgtcctggacagctggcaagcaatgtcgcaaacgtaagaagagctctatgcc 610

Qy   837 TCAGAAATTTCTTGGGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGA 896
         |||||||||||||| |||||   |||||||| ||||| || |||||| |||||||||| ||
Db   611 tcagaaatttcttggagacaagtgcctgtcagacagtgccaactatga 670
```

```
US-08-733-622C-15

Query Match             52.4%;  Score 813.2;  DB 4;  Length 1788;
Best Local Similarity   85.5%;  Pred. No. 1.9e-171;
Matches  983;  Conservative   0;  Mismatches 143;  Indels  24;  Gaps   6;

Qy    417  CACTGGAGAACGGCCCTTCAGTGCAATCAGTGCGGCGGCCTCATTCACCAGACAGAGGCAA  476
           ||||| |||||||||| ||||||||||| |||| |||||||||||  ||||||| |||||
Db    378  catgggtgaacggcctttccagtgcaaccagtctgggcctccttaccccagaaaggcaa   437

Qy    477  CCTGCTCCGGCACATCAAGCTGCATTCGGGGAGAAGCCCTTCAAATGCCACCTCTGCAA   536
           | | |||| ||||||||||||||||| |||| ||||||||||||||||||||  | |||
Db    438  cctcctgcggcacatcaagctgcactcggttgtgagaagcccttcaaatgccatcctttgcaa  497

Qy    537  CTACGGCTGCCGCCGGACGACGCCCTCACTGGCCACCTGAGGACGCACTCCGTTGGTAA   596
           ||| | ||||||||| |  | |||||||||||||||||||||||||||| ||||||| ||
Db    498  ctatgcgtgcgcgcgggaggggacccctcaccggcacctgaggacgcactccgttggtaa   557

Qy    597  ACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAAGCTCTTTAGAGGAACA   656
           |||||||||||||||||||||||||||||| |||||||||||||| ||||| |||||| |
Db    558  gcctcacaaatgtggatattgtggccggagctataaacagcgaagctcttagaggagca   617

Qy    657  TAAAGAGCGCTGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCACACTGTACCCAGT   716
           ||||||||| |||  |||||||||| |||||||||||||||||||||   | |||||||||
Db    618  taaagagcgatgtccacaacttacttgaaagcatgggccttccgggc---gtgtgccagt  674

Qy    717  CATTAAGAAGAGAAAACTAAGCACAGTGAAAATGGCAGAAGACCTGTCAAGATAGGATCAGA  776
           ||||||| || ||||| |||| |||| | |||  |||||| || ||||| ||||||||| |
Db    675  cattaagagaaacctaaccacaacgagatgcagagaccgtgcagataggagcaga       734

Qy    777  GAGATCTTCTGTGCTGACAGATAGCAGCTGCAAGCTGAAGTGTGCCAAACGTAAGAGCTCTATGCC  836
           || ||||||| ||||||||||| | || |||||  |||| |||||||| || | || ||||||
Db    735  gaggtcccttgtcctggacaggctggcaagcaatgtgcaaacgtaagagtctatgcc       794

Qy    837  TCAGAAATTCTTGGGGACAAGGGCTGTCCCACACGCCCCTACGACGCCATGACCAGTGCCACGTACGA  896
           ||||||  | || || |||||| |||||||| | |  ||| ||||||||||||||||||||||||
Db    795  tcagaaatttcttggagacaagtggct gttcagacatgcccatgaccagtgccaactatga     854

Qy    897  GAAGGAGGAACGAAATGATGAGTCCCACGTGATGGACCAAGCTGATGACCAAGCACCATCAA  956
           || || |||||| ||||| ||| || |||| | |||| ||||||| || |  |||||||||
Db    855  gaaggag---gatatgatgacatccacgtgaccgatgacaaccatgccatcaa           911

Qy    957  CTACCTGGGGCCGGCCCAGTCCCTGCTCGCGCCTGGTGCAGACCTGCACGACCGGCGGTTCCGAGGT  1016
           |||| |||||||| |||  |||||| ||||||||||||||||||||| |||||||||||||||||||
Db    912  ctacctggggccgtcccagtccctgctcgcgcctggtgcagacacccccgggtagtccgggt      971

Qy   1017  GGTCCCGGTCATCAGCCCGATGTACCAGCTGCACAGCGCG---CTCCGAGGGCACCCCCG  1073
           ||| |||| |||||||||| ||||||||||||| ||||||   |||| ||||||| || |
Db    972  ggttcccggtcatcagcccgatgtaccagctgcacagcgcggtcctcgagggcaccacccgcg  1031

Qy   1074  CTCCAACCACTGGCCGCGTGGAGTACCTGTGCTCTCCAAGGCCAA  1133
           |||||||||||||| | |||| |||||||| ||| | || |||||
Db   1032  gtccaaccattcagcacagga---cgccgtggataacttgctcgtgtccaaggccaa      1088

Qy   1134  GTTGGTGCCCTCCGGAGGCCGGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACAC  1193
           || |||||| ||| || ||| |||| ||| | |||| |||||||||||||||||||||||||
Db   1089  gtctgtgcatccgacgcggagcgtccgagttcgtggtcagcacgagctggcgagcagctgaa   1148

Qy   1194  CGAGAGCAACAACAGGAGGAGGAGCAGCGCAGCGCCGCGTGCAACCTGCACCATCGCCCCG  1253
           ||||||||||||| ||| |||| | |||||||||||| |  |||||  || ||||||||||
Db   1149  agagagcaacaacgcggaaccgggaccagcagcggccctatcccacctaaccaccacatcaaccc  1208

Qy   1254  ACGCGCGC---AACGCGTGTCGCTCAAGGAGGAGTCCCCGATGTACCAGCTGCCACAGCCG  1310
           | |||||    ||||||| |||| | |||| || |||||||||| ||||||| |||||||||
Db   1209  gcatgcacgcaatgggctggcctcaagaggagtcccccctacgaggtgctgagggc       1268

Qy   1311  CGCTCCGAGAACTCGCAGGACGCGTCCCGGCTCCAGAGTCTGCGCACATAACGGGAGCAGATGAA  1370
           ||||| |||||| || | ||  |||||| |||||| || |||||||||| |||||| |||||||
Db   1269  ggcctcagagaactcgcaggatgccttccgtgtcatcagcacgagtcgcgagcagtcgaa      1328

Qy   1371  GGTGTACAAGTGCCAACACTGCCGGTGCTCTTCCTGGATCACGTCATGTACACCATCCA  1430
           ||||||||||||||||||||||||| ||||||| |||||||| | | | ||||||||||
Db   1329  ggtgtacaagtgccaacactgccggtgctcttcctggatcacgtcatgtacaccatcca       1388

Qy   1431  CATG-------GGTCGCCACGCTTCCGTGATCCTTTGAGTGCAACATGTGCGGCTA  1481
           ||||       |  | | || || ||||||  | | |||||||||||||||||||||
Db   1389  catgggtgcccatggggctcgtgcctccatggctgttccggttcggatatctgtgtaacatgtgtggctta  1264? 1448

Qy   1482  CCACAGCCAGGACGTTCGTGCGCACATAACGGAGGGGAGCACCGCTTCA  1541
           ||||||  |||||| |  |  ||||||| |||||||||||  |||| |||
Db   1449  tcacagccaggacagtacgagttctcatcaccatcccatatcacgcgggggggagcatcgttacca  1324

Qy   1542  CATGAGCTAA  1551
           ||||||| ||
Db   1325  cctgagctaa  1334
```

```
RESULT 11
US-08-733-622C-15
; Sequence 15, Application US/08733622C
; GENERAL INFORMATION:
;  APPLICANT: Georgopoulos, Katia
;  APPLICANT: Morgan, Bruce A.
;  TITLE OF INVENTION: AIOLOS GENE
;  FILE REFERENCE: 10287-030001
;  CURRENT APPLICATION NUMBER: US/08/733,622C
;  CURRENT FILING DATE: 1996-10-17
;  PRIOR APPLICATION NUMBER: US 60/017,646
;  PRIOR FILING DATE: 1996-05-14
;  PRIOR APPLICATION NUMBER: US 60/005,529
;  PRIOR FILING DATE: 1995-10-18
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 15
;  LENGTH: 1788
;  TYPE: DNA
;  ORGANISM: Mus musculus
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (223)...(1515)
```

```
Db   1329 ggtgtacaagtgcgaacactgccgcgtgctcttcctggatcacgtcatgtataccattca 1388
               ||||||| |||||| |||||||||||  ||||||| ||||| ||| |||||||||||
Qy   1431 CATG------GGCTGCCACGGCTTCCGTGATCCTTTGAGTGCAACATGTGCCGCTA 1481
               ||||      |||||| ||||| || ||||| ||| ||| || ||| ||||| || ||
Db   1389 catgggctgccatggctgccatgtctcggatccttcggatcctttggagtgtaacatgtggtta 1448
Qy   1482 CCACAGCCAGGACCCGGTACGAGTTCTCGTGCCACATAACCGGAGGGAGCACCGGCTTCCA 1541
               |||||||||| |||||||||||||||| || ||| |||||  || ||  || ||| || |||
Db   1449 tcacagccaggacggtacgagttctcatcccatatcacgcggggggagcatcgttacca 1508

Qy   1542 CATGAGCTAA 1551
               | ||||||||
Db   1509 cctgagctaa 1518

RESULT 12
US-08-733-622C-17
; Sequence 17, Application US/08733622C
; GENERAL INFORMATION:
;  APPLICANT: Georgopoulos, Katia
;  APPLICANT: Morgan, Bruce A.
;  TITLE OF INVENTION: AIOLOS GENE
;  FILE REFERENCE: 10287-030001
;  CURRENT APPLICATION NUMBER: US/08/733,622C
;  CURRENT FILING DATE: 1996-10-17
;  PRIOR APPLICATION NUMBER: US 60/017,646
;  PRIOR FILING DATE: 1996-05-14
;  PRIOR APPLICATION NUMBER: US 60/005,529
;  PRIOR FILING DATE: 1995-10-18
;  NUMBER OF SEQ ID NOS: 38
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17
;  LENGTH: 1296
;  TYPE: DNA
;  ORGANISM: Mus musculus
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(1296)
US-08-733-622C-17

Query Match         44.4%;  Score 689.4;  DB 4;  Length 1296;
Best Local Similarity   72.0%;  Pred. No. 6.3e-144;
Matches 1125;  Conservative   0;  Mismatches 156;  Indels 282;  Gaps   6;

Qy      1 ATGGATGCTGACGAGGTCAAGACATGTCTTTCTCATCAGGGAAGGAAAGCCCCCTGTA 60
           |||| || |||||||||||||||  |||| |||||||||||||||||||||||||
Db      1 atggatgtcgatgaggtcaagacatgtcccaagtttcaggaaaggagagcccccagtc 60

Qy     61 AGCGATACTCCAGATGAGGGCGATGAGCCCATGCCGATCCCGAGGACCTTCTCCACCACC 120
           ||||| ||||||||| ||| |  ||| ||||||| ||| ||||| ||||| ||||| |||
Db     61 agtgacactccagatgaaggggatagcccatgcctgctgcctgccctgtcctcctggacctgtcccactacc 120

Qy    121 TCGGAGGACGACAAAGCTCCAAGAGTGACAGAGTCTGTGGCCAGTGACAGTCTAAAGTAG 180
           |||| |||| ||||||||  | ||||||||||||| || ||||||| ||||||||||
Db    121 tctggaggacgacgagcagaactccaagagtgatgtgagggcatggccagtgccagtaaagtaagtagag 180

Qy    181 ACTCAGAGTGATGAAGAAGAATGGCGTGCCTGTGAAATGAATGGGGAAGAATGTGCGGAG 240
           |||||||| |||||| ||||| |  ||| |||||| |||||||||||| ||||||  ||
Db    181 actcagagtgatgaagaagaatggcgtgcctgtgaaatgaatgggggaagaatgtgcagag 240

Qy    241 GATTTACGAATGCTTGATGCCTCGGAGAGAAAATGAATGGCTCCCACAGGGACCAAGGC 300
           ||||| |||| ||||| |||||| |||||||| || ||||| ||| ||||||| |||||
Db    241 gatttacgaatgcttgatgcctcgggagagaaaatgaatggctcccacagggaccaaggc 300

Qy    301 AGCTCGGCTTTGTCGGGAGTTGGAGGCATTCGACTTCCTAACGAAAACTAAAGTGTGAT 360
           |||||| ||  ||||||| |||||||| |||| |||||||| ||||| ||||||
Db    301 agctcggcttttgtcggggttggaggcattcgacttcctaacgaaaacttaaagtgtgat 360

Qy    361 ATCTGTGGGATCATTTGCATCGGGCCCAATGTGCTCATGGTTCACAAAAGAAGGCCACACT 420
           ||||||||||| || |||| ||||| |||| |||  |||||||||| || || ||  ||
Db    361 atctgtgggatcgttttgcatcgggcccaatgtgctcatggttcacaaaaggaagtcatact 420
```

```
Qy    421 GGAGAACGGCCCTTCCAGTGCGCAATCAGTGCGGGGCCTCATTCACCCAGAAGGGCAACCTG 480
           || |||||| ||||||||||| |||||||  |||| ||||||| || |||||||| ||||||
Db    421 ggtgaacggccctttccagtgcgcaaccagtctgggcctcctttaccagaaagggcaacctc 480

Qy    481 CTCCGGCCACATCAAGCTGCATTCCGGGAGAAGCCCTTCAAATGCCACCTGTGCAACTAC 540
           ||||| |||| ||||| || |||||| |||| ||||  ||||||| |||||||||||| ||
Db    481 ctgcggcacatcaagctcgacactcttgagtgcatcttgtcaactat 540

Qy    541 GCCTGCCGCCGGAGGACGACCCTCACTGGCCACTGAGGACGCACTGCACTCCGTTGGTAAACCT 600
           |||||||||||||||||| |||||||| ||||| ||||||||| ||||||||||||||
Db    541 gcctgccgcgcggaggacgcccctcaccggccacctgaggacgcactcc-----  588

Qy    601 CACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAAGCGTCTTTAGAGGAACATAAA 660
Db    589 -----------------------------------------------------------  588

Qy    661 GAGCGCTGCCACAACTACTTGGAAGCATGGCCTTCCGGGCCACACTGTACCCAGTCATT 720
           |||| ||||| ||||||||||||||||||||||||||||||||||||||| |||||| ||
Db    589 -----------------------------------------------------------  588

Qy    721 AAAGAGAAACTAAGCACACAGTGAAATGGCAGAAGACCTGTCAAGATAGGATCAGAGAGA 780
Db    589 -----------------------------------------------------------  588

Qy    781 TCTCTCGTGTCTGGACAGACTAGCAAGTAATGTCGCCAAACGTCTGTATGCCTCAG 840
Db    589 -----------------------------------------------------------  588

Qy    841 AAATTTCTTGGGACAAGGCCGTGTCCGACACGCCGTGTCCACGTACGAGAAG 900
           || ||||||||| |||||| ||| ||||||| ||||||||||| || |||||
Db    589 --------ggagacaagtgcctgtcagacatgccctatgacagtgcaactatgagaag 639

Qy    901 GAGAACGAAATGATGAAGTCCACCGTGATGGACCAAGCCCATCAACACGCCATCAACTAC 960
           |||   ||  ||   ||||||||| ||||||| ||||||| |||||||||| ||||||
Db    640 gag---gatatgatgacatcccacgtggacaggccatcaacaatgccatcaactac 696

Qy    961 CTGGGGGCCGAGTCCTGCCCCCGGTGTCAGAGCCGCCCCCGGCGGTTCCGAGGTGGTC 1020
           |||||| ||  |||||||||||||||  || |||| ||||||||||| ||||||||||
Db    697 ctggggctgagtccctgcccgtgtcagcagacaccccggtagctccgaggtggtg 756

Qy   1021 CCGGTCATCAGCCCGATGTACCAGTGCACAGG----CGGTCGGAGGGCACCCGGCTCC 1077
           ||||||||||| |||||||| || |||||| ||| ||| ||| | || || ||||||||
Db    757 ccagtcatcagctccatgtaccagtgcacaagcaccccctcagatggcccccacggtcc 816

Qy   1078 AACCACTCGGCCACCGGGGCCGGGAGTACCTGCTGCTCCTCCAAGGCCAAGTTG 1137
           ||||| || ||||||||||| ||||  |||| |||| || ||||||| ||||||||
Db    817 aaccattcagccacgga---cgccgtggataacttgctgctgctgccaaggccaagtct 873

Qy   1138 GTGCCCTCGGAGCGCGGAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGGACCGAG 1197
           |||||||||| ||| |||||||||||| |||||||||| ||| ||| || |||
Db    874 gtgtcatcggaggcggaggaggcctcccgagcaacagctccaagactccacagatacagag 933

Qy   1198 AGCAACAACGAGGAGGCAGCGGGAGCTCTTACCTGACCAACCACATCGCCCGACGC 1257
           |||||||  |||||| ||| ||| |  |||||||| || ||||||||||||| |||
Db    934 agcaacgcggaggaacagcggcagcggccttatctacctaaccaccacatcaaccgcgat 993

Qy   1258 GCGCG---AACCGCTGCGTCAGGAGGAGCAGCAGCGCCTACGACCTGCGCGCCGCC 1314
           || |    || ||| ||| | || ||  ||||| ||||| || || ||| || ||||
Db    994 gcacgcaatggctcggctctccaaggaggagcgcgccgaggtgctgagggcggcc 1053

Qy   1315 TCCGGAACTCGCAGGACGTGTCAGTGGGGCGGGGAGCCAGATGGAAGGTG 1374
           ||||| |||| | ||| || |||||||  ||||||||| || ||||||| ||
Db   1054 tcagagaactcgcaggatgcctccgtggtcagcacgagtggcgagcagctgaaggtg 1113

Qy   1375 TACAAGTGCCAACACGCCGGAACTCCTAACGAAAACTAAACTAAAGTGTGAT 1434
           ||||| |||| |||||| ||| ||| ||||| ||||| |||||||| |||||
Db   1114 tacaagtgcgaacactgccgcgtgctctcctggatacacgtatcacattcacatg 1173

Qy   1435 -------GGCTGCCACGGCTTCCGTGATCCTTTGAGTGCAACATGTGCGGCTACCAC 1485
                  ||||||| || |||| ||||| ||| | ||| |||||| || || |||| ||
Db   1174 ggctgccatggctgccatggcttcggatcccttggttgtacatggtggttatcac 1233

Qy   1486 AGCCAGGACCGGTACGAGTTCTCGTGCCACATAACGGGAGCACCGGCTTCCACATG 1545
```

```
Db  1234  agcaggacaggtacgagttctcatcccatatcacgcgggggggagcatcgttaccacctg  1293
           |||||||| |||||||||||||| || || |||||| |||||||| || | |||| ||

Qy  1546  AGC  1548
           |||
Db  1294  agc  1296


RESULT  13
US-08-733-622C-19
; Sequence 19, Application US/08733622C
; GENERAL INFORMATION:
;  APPLICANT: Georgopoulos, Katia
;  APPLICANT: Morgan, Bruce A.
;  TITLE OF INVENTION: AIOLOS GENE
;  FILE REFERENCE: 10287-030001
;  CURRENT APPLICATION NUMBER: US/08/733,622C
;  CURRENT FILING DATE:  1996-10-17
;  PRIOR APPLICATION NUMBER: US 60/017,646
;  PRIOR FILING DATE: 1996-05-14
;  PRIOR APPLICATION NUMBER: US 60/005,529
;  PRIOR FILING DATE: 1995-10-18
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  NUMBER OF SEQ ID NOS: 38
;  SEQ ID NO 19
;   LENGTH: 1170
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;    NAME/KEY: CDS
;    LOCATION: (1)...(1170)
US-08-733-622C-19

Query Match            37.2%;   Score 577;  DB 4;  Length 1170;
Best Local Similarity  75.4%;   Pred. No. 6.2e-119;
Matches   865;  Conservative    0;  Mismatches  135;    Indels  147;   Gaps    6;

Qy  417  CACTGGAGAACGGCCCTTCCAGTGCAATCAGTGCGGGCCCTCATTCACCCAGAAGGGCAA  476
          || || |||||||| |||||||| |||  ||||| ||||||||| || |||||| ||||
Db  156  catgggtgaacggcctttccagtgcaaccagtctgggcctccctttacccagaaaggcaa  215

Qy  477  CCTGCTCCGGCACATCAAGCTGCATTCCGGGGAGAAGCCCTTCAAATGCCACCTTCGCAA  536
          | ||||||||||||||| || |||||||| || |||||||||| || ||| |||| ||
Db  216  cctcctgcggcacatcaagctgcactcggttgagagcccctcaaatgccatctttgcaa  275

Qy  537  CTACGGCCTGGCCCGCGGACGGCCCCTCACTGGCCTGCCCACCTGAGGACGGCCACTCCGTTGGTAA  596
          || |||||||||||| |||||||||||||||||||  | |||||||||||||||||||
Db  276  ctatgctgctgccgcgggaggagcgcccctcaccggcacctgaggacggcactcc------  327

Qy  597  ACCTCACAAATGTGGATATTGTGGCCGAAGCTATAAACAGCGAACGTCTTTAGAGGAACA  656
          ||||||||||||||||  ||||||||||||||| ||||||  ||| || | |||||||
Db  328  ------------------------------------------------------------  327

Qy  657  TAAAGAGCGCCGTGCCACAACTACTTGGAAAGCATGGGCCTTCCGGGCACACTTGTACCCAGT  716
          |||||||||| | |||||||||||| || |||||||| |||||| || |||||||||
Db  328  ------------------------------------------------------------gt  329

Qy  717  CATTAAAGAAGAAAACTAAGCACAGTGAAAATGGCAGAAGACCTGTCCAAGATAGGATCAGA  776
          ||||||| ||||||| ||| || |||||||||||||||||||||||||||| |||||
Db  330  cattaaggaagaaactaaccaacagagatggcaagaggtgcaagataggaggcaga  389

Qy  777  GAGATCTTCGTGTCGTGACAGACTAGCAAGTAATGTCGCCAAACGTAAGAGCTCTATGCC  836
          || || |||||||||||| | |||||| |||| | |||||||||||||||||||
Db  390  gaggtccttgtcctgacagcaggctgacaagctaggagctctatgcc  449

Qy  837  TCGAAATTTCTTGGGGACAAGGGCCTTCTGTCCGACACGCCCTACGACAGTGCCACGTACGA  896
          |||||| |||| |||||||| || || |||| |||||||||| || |||||
Db  450  tcagaaatttcttggagacaagtgcctgtcgtcagacatgcccatgacagtgccaactatga  509

Qy  897  GAAGGAGGAACGAAATGATGAAGTGAAGACTCCCACGTGATGACCAAGGCCATCAACAACACGCCATCAA  956
          |||||| | ||||||| |||||||||||||||||||||||||||||||||||||||
Db  510  gaaggag---gatatgatgacatcccacgtgatgaccaggccatcaacaatgccatcaa  566
```

                                                                                                                          1016
```
Qy  957   CTACCTGGGGGCCCAGTCCTGCCCTGCCGCCCCCGGGGCGGTTCCGAGGT
           |||||||||| |||||||||||| |||||||||||||||| || | |||||||
Db  567   ctacctggggctgagtccctgcccattggtgcagacaccccccggtagctccgaggt  626

Qy  1017  GGTCCCGGTCATCAGTCCCGATGTACCAGCTGCACAGG---CGCTCGGAGGGCACCCGCG  1073
           ||| ||| || ||||||  | |||||||||||||||||   || || ||||||||||||
Db  627   ggtgccagtcatcagctccatgtaccagctgcacaagcgccccctcagatgccccccacg  686

Qy  1074  CTCCAACCACTCGGCCCAGGACACGCCGCGGAGTACCTGCTGCTCTCCAAGGCCAA  1133
           ||||||| || ||| |||||   || ||||  | |||||||||| ||||||||
Db  687   gtcaaccattcagcacagga---cgccgtggataacttgctgctgtccaaggccaa  743

Qy  1134  GTTGGTGCCTCGGAGCGCGGAGGCGTCCCGAGCAACAGCTGCCAAGACTCCACGGACAC  1193
           ||||||||| ||||||| |||||||||| |||||||| || ||||||| |||||||
Db  744   gtctgtgtcatcggaggcgagaggcctcccggcaacagctgccaagactccacagatac  803

Qy  1194  CGAGAGCAACAACGAGGAGGAGCAGCGACGCGTCTTATCTACCTGACCAACCACATCGCCCG  1253
           |||||||| |||||| |||||||||||||||| ||  ||||| |||||||||||||| ||
Db  804   agagagcaacgcgggaggaacagcagcgaccggcctatcctatctacctaaccaacacatcaaccc  863

Qy  1254  ACGCGCGC---AACGGCTGTCGCTCAAGGAGGAGCAGCCACCGGCTACGACCTGCTGCGCGGC  1310
           | ||| | | | |||||| |||||||||||||||||||||||| |||||
Db  864   gcatgcacgcaatgggctgctcctcaaggaggagcagccgagtgccgagagcatgcgagggggc  923

Qy  1311  CGCCTCCGAGAACTCGCAGACGACGGCCTCCCGTGGTCAGCACCAGCGGGAGCAGATGAA  1370
           | ||||||||||| |||| ||||||||| ||||||| |||||| ||| |||||||||||
Db  924   ggcctcagagagaactcgcaggatgcctccggtcagtgagtggcgagcagctgaa  983

Qy  1371  GGTGTACAAGTGCGAACACTGCCGGGTGCTTCTCCTGGATCACGTCATGTACACCATCCA  1430
           |||||||||||||||||||||||||||  || ||||| |||||| |||||| || |||||
Db  984   ggtgtacaagtgcgaacactgccgtgctcttcctggatcacgtcatgtataccattca  1043

Qy  1431  CATG--------GGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTA  1481
           ||||        |||| |||||||||||| || ||  |||||| || ||||| |||| ||
Db  1044  catgggtcgcatggtgccatggcttcggatccctttgagtgtaacatgtgtggtta  1103

Qy  1482  CCACAGCCAGGACCAGGACGTACGAGTTCTCGTGCCACATAACGCGGAGGGAGCACCGCTTCCA  1541
           |||||||| ||||||||| ||||| ||||  | || |||||||||||||||||||||||||
Db  1104  tcacagccaggacaggtacgagttctcatcatcccatcacgcggggggggagcatcgttacca  1163

Qy  1542  CATGAGC  1548
           | |||||
Db  1164  cctgagc  1170


RESULT  14
US-10-035-832-1157
; Sequence 1157, Application US/10035832
; GENERAL INFORMATION:
;  APPLICANT: Morris, David
;  APPLICANT: Engelhard, Eric
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR CANCER
;  FILE REFERENCE: A-71249/RMS/DCF
;  CURRENT APPLICATION NUMBER: US/10/035,832
;  CURRENT FILING DATE:  2002-07-22
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 1613
;  SOFTWARE: PatentIn version 3.1
;  SEQ ID NO 1157
;   LENGTH: 87977
;   TYPE: DNA
;   ORGANISM: Mus musculus
;   FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (2001)..(2048)
;    OTHER INFORMATION: "n" at positions 2001 thru 2048 can be any base
;   FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (6720)..(7498)
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;   OTHER INFORMATION: "n" at positions 6720 thru 7498 can be any base
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (8834)..(8882)
;   OTHER INFORMATION: "n" at positions 8834 thru 8882 can be any base
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (16167)..(16186)
;   OTHER INFORMATION: "n" at positions 16167 thru 16186 can be any base
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (24443)..(24580)
;   OTHER INFORMATION: "n" at positions 24443 thru 24580 can be any base
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (28778)..(28871)
;   OTHER INFORMATION: "n" at positions 28778 thru 28871 can be any base
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (45952)..(46750)
;   OTHER INFORMATION: "n" at positions 45952 thru 46750 can be any base
US-10-035-832-1157


Query Match       30.9%;    Score 479.2;  DB 6;   Length 87977;
Best Local Similarity  83.8%;    Pred. No. 5.6e-97;
Matches  593;   Conservative   0;   Mismatches  103;   Indels   12;   Gaps   4;

Qy    850 GGGGACAAGGGCCGTGCCGACACGCCTACGACAGTGCCACGTACGAGAAGGAGAACGAA  909
          || ||||| |||||| |||| |||| ||||||| |||||| ||||||||| ||||||||
Db  77059 ggagacaagtgcctgtcagacatgccactgccaactatgagaaggag--gat 77115

Qy    910 ATGATGAAGTCCCACGTGATGGACCAAGCCATCAACACAACGCCATCAACTACCTGGGGCT  969
          ||||| |||||||||||| ||||||||| ||| ||||| |||| ||||||||||||||||
Db  77116 atgatgacatcccacgtgatggaccaagcaatcaacaatgccatcaactacctgggggct 77175

Qy    970 GAGTCCCTGCGCGCCGCTGGTGCAGACGCCCCGGGGCGGTTCCGAGGTGGTCCCGGTCATC 1029
          |||||||||||||||||||| ||||| |||||| || || ||||||||||||||||||
Db  77176 gagtccctgcgcgcccattggtgcagacaccccggtgctccgaggtggtgccagtcatc 77235

Qy   1030 AGCCCGATGTACCAGCTGCACAGG---CGCTCGGAGGGCACCCCGCCTCCAACCACTCG 1086
          ||| ||||||||||||||||||    | || ||||||| || |||||||||||||||||
Db  77236 agtccatgtaccagctgcacaagcccctcagatggcccccacggtccaacaattca 77295

Qy   1087 GCCCAGGACAGCCGCGTGGAGTACCTGCTGCTCCAAGGCCAAGTTGGTGCCCTCG 1146
          || ||||| |||||||||||||||||||| |||||||||||| || |||||||||
Db  77296 gcacagga---cgccgtggataacttgctgctgctgccaagcaagtctgttgtcatcg 77352

Qy   1147 GAGCGCGAGGCGGTCCCCGAGCAACAGCTGCCAAGACTCCACGGACACCGAGCACAAAC 1206
          |||| ||||| ||||||||||||| |||||| |||||||||||||||||||||||||||
Db  77353 gagcgagaggcctcccccgagcaacagctgccaagactccacgagagagcaacgcg 77412

Qy   1207 GAGGAGCAGCCAGCGGTGGTCTTATCTACCTGACCAACCAACCACCACATCGCCCGAGAAC 1263
          |||||||||||||||||||||||  |||| |||||||||||||||||||||| |||||
Db  77413 gaggaacagcgcagcggccttatctacctaaccaacaaccacatgccgcacgcaat 77472

Qy   1264 CGCCTGTCGCTCAAGGAGGACCACCGCCCTACGACCTGCTGCGCGCCCTCCGAGAAC 1323
          || ||||| ||||||||||||||||||||||| | |||| |||| ||| |||||||
Db  77473 gggctggctcaaggaggagcagcgcgctacggaggtgcggcggcctcagagaac 77532

Qy   1324 TCGCAGGACGCGCTCCCGCGTGGTCAGCACGACCAGCGGGGAGCAGATGAAGGTGTACAAGTGC 1383
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  77533 tcgcaggatgccttccgtggtcagcacgacgagtggcgagcagctgaaggtgtacaagtg 77592

Qy   1384 GAACACTGCCGCGGGTGCTTCTCCTGGATCACGTCATGTGCAACATCCACATGGGCTGCCAC 1443
          ||||||||||| ||||| || |||||||||| ||||| || |||| |||||||||||||||
Db  77593 gaacactgccgcgggtgctctccggatcacgtcatgtataccaccatcacatgggctgccat 77652

Qy   1444 GGCTTCCGTGATCCTTTTGAGTGCAACATGCGGGCTACCAGCGACCAGGACCGTACGAG 1503
          ||||| || |||||| ||||||||||| ||| ||||||||||||||||||| |||||||
Db  77653 ggcttcgggatccctttgagtgtaacatgtggttatcacagccaggacaggtacgag 77712

Qy   1504 TTCTCGTCCGCACATAACGCGAGGGGAGCCACCCGCTTCCACATGAGCTAA 1551
          ||||||||||||||||||||||||||||||||||||||||||||||||||
Db  77713 ttctcatcccatcacgcgggggggagcatcgttaccacctgagctaa 77760


RESULT 15
US-08-733-622C-20
;  Sequence 20, Application US/08733622C
;  GENERAL INFORMATION:
;  APPLICANT: Georgopoulos, Katia
;  APPLICANT: Morgan, Bruce A.
;  TITLE OF INVENTION: AIOLOS GENE
;  FILE REFERENCE: 10287-030001
;  CURRENT APPLICATION NUMBER: US/08/733,622C
;  CURRENT FILING DATE:   1996-10-17
;  PRIOR APPLICATION NUMBER: US 60/017,646
;  PRIOR FILING DATE:   1996-05-14
;  PRIOR APPLICATION NUMBER: US 60/005,529
;  PRIOR FILING DATE:   1995-10-18
;  NUMBER OF SEQ ID NOS: 38
;  SEQ ID NO 20
;  LENGTH: 1128
;  TYPE: DNA
;  ORGANISM: Mus musculus
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (1)...(1128)
US-08-733-622C-20


Query Match       29.5%;    Score 458.2;  DB 4;   Length 1128;
Best Local Similarity  82.7%;    Pred. No. 1.7e-92;
Matches  591;   Conservative   0;   Mismatches  103;   Indels   21;   Gaps   5;

Qy    849 TCGGGACAAGGGCCTGTCCGACACGCCCTACGACAGTGCCACGTACGAGAAGGAGAACGA  908
          ||||||| |||||| ||||| |||| ||||||| ||||||||| ||||||||||||||
Db    420 tggagacaagtgcctgtcagacatgccaactatgagaaggag--ga 476

Qy    909 AATGATGAAGTCCCACGTGATGGACCAGCCATCAACAACGCCATCAACTACCTGGGGGC  968
          |||||||||||| |||||||||||||||| |||||| ||||||||||||||||||||||
Db    477 tatgatgacatcccacgtgatgatggaccatcaacaatgccatcaactacctgggggc 536

Qy    969 CGAGTCCCTGCGCGCCGCCGGTGTCAGACGCGCCCCGGGCGGTTCCGAGGTGGTTCCGGTCAT 1028
          |||||||||| ||||||||||| ||||||||||||||||||||||||||||||||||||
Db    537 tgagtccctggcgccattggttcagacacccccggtagctccgaggtggtgccagtcat 596

Qy   1029 CAGCCCGATGTACCAGCTGCACAGG---CGCTCGGAGGGCCACCCCGCCTCCAACCACTC 1085
          ||||||||||||||||||||||||    || |||||||| ||||||||||||||||||
Db    597 cagctccatgtaccagctgcacaagcccctcagatggccccccacggtccaacaattc 656

Qy   1086 GGCCCAGGACAGCCGCGTCGGAGTACCTGCTGCTCCTCCAAGGCCAAGTTGGTGCCCTC 1145
          || |||||| | ||||| |||||| ||||| |||| ||||| ||||| || |||||||
Db    657 agcacagga---cgccgtggataacttgctgctgtctgccaagtctgtcatc 713

Qy   1146 GGAGCGCGAGGCGTCCCCGAGCAACAGCTGCCAAGACTCCACGGAGAGAGCAACAA 1205
          |||||| ||||| | |||||||||||||||| ||||||||||| || |||||||||
Db    714 ggagcgagaggcctccccccgagcaacagctgccaagatacagagagcagcgc 773

Qy   1206 CCGAGGAGCAGCCAGCGGTCTTATTCTACCTGACCAACCAACCACCACATCGCCCGAGCGCGC---A 1262
          |||||||||||||| |||||| | | |||| |||||||||||||||||||| | | ||||
Db    774 ggaggaacagcgcagcggcttatctatccacctaacctaccacatcaacccgcatgcacgcaa 833

Qy   1263 ACGCGTGCTGCTCAAGGAGGAGCACCGCCCTACGACCTGCGCGCCTCCGAGAA 1322
          | | |||| |||||||||| ||||||||||||| | | ||| |||| |||
Db    834 tgggctggctctcaaggaggagcagcgcgcctacgaggtgctgagggcggcctcagagaa 893

Qy   1323 CTCGCAGGACGCGCTCCCGCGTGGTCAGCACCACCAGCGGGGAGCAGATGAAGGTGTACAAGTG 1382
          |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Db    894 ctcgcaggatgccttccgtggtcagcacgacgagtggcgagcagctgaaggtgtacaagtg 953

Qy   1383 CGAACACTGCCGCGGGTGCTTCTCCTGGATCACGTCGATCACCTCATCTAACTACCACATG------ 1434
          ||||||||||||||||||||||||||||| ||||||||||| |||| |||||||||||||
Db    954 cgaacactgccgcgggtgctctccggatcacgtcatgtataccattcacatgggctgcca 1013
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Qy   1435  -GGCTGCCACGGCTTCCGTGATCCTTTTGAGTGCAACATGTGCGGCTACCACAGCCAGGA 1493
                ||||||||| ||||| || ||||| ||||| |||||||| |||||| || || |||||||||||
Db   1014  tggctgccatggctttcgggatcccttgagtgtaacatgtgtggttatcacagccagga 1073

Qy   1494  CCGTACGAGTTCTCGTCGCACATAACGCGAGGGAGCCACCGCTTCCACATGAGC 1548
                | |||||||||||||| || || ||||| |||||| |||| | ||||||| |||||
Db   1074  caggtacgagttctcatcccatatcacgcgggggagcatcgttaccacctgagc 1128
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Search completed: August 28, 2002, 09:59:37
Job time: 5027 sec